

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 03:29:34 ; Search time 6787 Seconds
(without alignments)
13011.508 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1131	48.8	1182	9	AY404343	AY404343 Homo sapi
2	754	32.5	759	7	CN396938	CN396938 170004177
3	725	31.2	879	5	BQ216829	BQ216829 AGENCOURT
4	563	24.3	916	6	CD050395	CD050395 AGENCOURT
5	457	19.7	510	7	CN396939	CN396939 170005999
c 6	430	18.5	430	1	AI917116	AI917116 ts52a02.x
c 7	422	18.2	422	1	AI580389	AI580389 tm42f08.x
8	395	17.0	481	6	CB158774	CB158774 K-EST0218

c	9	373	16.1	439	1	AA633698	AA633698	ag87a11.s
	10	345	14.9	901	4	BI827790	BI827790	603075472
c	11	328	14.1	462	5	BX109306	BX109306	BX109306
	12	305	13.1	360	5	BP431975	BP431975	BP431975
c	13	294	12.7	1055	1	AI654867	AI654867	wb65c12.x
	14	290	12.5	460	7	R19994	R19994	yg38h02.r1
c	15	286	12.3	363	2	BF510946	BF510946	UI-H-BI4-
	16	285	12.3	342	5	BP431877	BP431877	BP431877
c	17	270	11.6	357	1	AA747964	AA747964	nx79a08.s
	18	268	11.6	1180	9	AY404344	AY404344	Pan trogl
c	19	254	10.9	543	2	AW236852	AW236852	xm49h11.x
c	20	220	9.5	429	2	AW236558	AW236558	xm47g07.x
c	21	181	7.8	361	1	AA730192	AA730192	nw41a02.s
	22	181	7.8	375	1	AA715548	AA715548	nv53g11.r
	23	175	7.5	349	7	F06529	F06529	HSC1BC021 n
c	24	170	7.3	363	7	Z39483	Z39483	HSC1BC022 n
	25	167	7.2	371	2	BE843851	BE843851	RC0-TN007
c	26	105	4.5	580	8	AQ059652	AQ059652	CIT-HSP-2
	27	68	2.9	419	7	CR740722	CR740722	CR740722
c	28	68	2.9	449	1	AI217703	AI217703	qh15e09.x
c	29	68	2.9	454	1	AA970255	AA970255	op64h06.s
c	30	68	2.9	470	1	AA974327	AA974327	oq10g06.s
c	31	68	2.9	478	1	AI015041	AI015041	ov51a05.s
	32	68	2.9	552	7	CV029784	CV029784	8702 Full
c	33	68	2.9	694	2	AW173071	AW173071	xj82g11.x
	34	65	2.8	771	7	CR767782	CR767782	DKFZp469C
c	35	59	2.5	436	8	AQ476159	AQ476159	CITBI-E1-
	36	59	2.5	531	8	AQ386013	AQ386013	RPCI11-14
	37	59	2.5	751	8	AQ748070	AQ748070	HS_5538_A
c	38	55	2.4	583	1	AI694348	AI694348	wd45g04.x
	39	52	2.2	555	5	BP332215	BP332215	BP332215
c	40	47	2.0	253	1	AI373521	AI373521	qz46f08.x
c	41	47	2.0	253	1	AI492912	AI492912	qz42f01.x
c	42	47	2.0	288	2	AW235540	AW235540	xn19d12.x
c	43	47	2.0	328	1	AI671780	AI671780	wa05h05.x
c	44	47	2.0	331	1	AI613123	AI613123	ty71h04.x
c	45	47	2.0	332	1	AI672388	AI672388	ty64f01.x
c	46	47	2.0	345	2	AW779709	AW779709	hn84f05.x
c	47	47	2.0	347	1	AI767712	AI767712	wh38h05.x
	48	47	2.0	380	7	CR746104	CR746104	CR746104
	49	47	2.0	383	5	BX955526	BX955526	DKFZp781A
c	50	47	2.0	405	1	AI433413	AI433413	ti65c03.x
	51	47	2.0	459	5	BX951484	BX951484	DKFZp781F
	52	47	2.0	578	5	BP275078	BP275078	BP275078
	53	47	2.0	582	5	BP274546	BP274546	BP274546
	54	47	2.0	585	7	CR770709	CR770709	DKFZp469J
	55	47	2.0	717	7	CR769328	CR769328	DKFZp469O
	56	47	2.0	761	4	BI559553	BI559553	603252894
c	57	42	1.8	148	2	BF089587	BF089587	CM2-HT094
c	58	42	1.8	599	1	AA758115	AA758115	ah68d01.s
c	59	38	1.6	619	9	CE584093	CE584093	tigr-gss-
c	60	37	1.6	291	1	AI521956	AI521956	ti79e06.x
	61	37	1.6	565	4	BI538734	BI538734	434264 MA
c	62	37	1.6	659	6	CB435346	CB435346	615435 MA
c	63	37	1.6	706	9	CE140389	CE140389	tigr-gss-
c	64	37	1.6	799	7	CK848020	CK848020	970722 MA
c	65	35	1.5	82	1	AA974589	AA974589	op28h10.s

	66	29	1.2	209	7	CR746121	CR746121	CR746121
c	67	29	1.2	455	2	AW380602	AW380602	RC2-HT027
	68	29	1.2	1021	7	CK231266	CK231266	ILLUMIGEN
c	69	28	1.2	566	6	CB433850	CB433850	610302 MA
c	70	28	1.2	580	6	CB423692	CB423692	597208 MA
c	71	27	1.2	641	6	CD634229	CD634229	56006284H
	72	26	1.1	136	1	AA073542	AA073542	mm94b03.r
	73	26	1.1	361	1	AA730192	AA730192	nw41a02.s
c	74	26	1.1	375	1	AA715548	AA715548	nv53g11.r
	75	26	1.1	399	1	AA245658	AA245658	mx03a06.r
	76	26	1.1	428	8	AQ194654	AQ194654	RPCI11-48
	77	26	1.1	453	1	AA245657	AA245657	mx03a05.r
	78	26	1.1	473	2	BF659710	BF659710	maa23c04.
	79	26	1.1	536	2	AW226792	AW226792	um62c04.y
	80	26	1.1	538	4	BG971731	BG971731	602838268
	81	26	1.1	551	2	BF785590	BF785590	602112377
	82	26	1.1	638	4	BI103514	BI103514	602889055
	83	26	1.1	660	2	BB221592	BB221592	BB221592
	84	26	1.1	711	2	BF785562	BF785562	602112344
	85	26	1.1	713	4	BI327590	BI327590	602979770
	86	26	1.1	721	4	BG972539	BG972539	602841125
	87	26	1.1	724	6	CB952493	CB952493	AGENCOURT
	88	26	1.1	738	6	CB954127	CB954127	AGENCOURT
	89	26	1.1	758	4	BI332502	BI332502	602981312
	90	26	1.1	772	4	BI099719	BI099719	602884581
	91	26	1.1	776	2	BF781397	BF781397	602104580
	92	26	1.1	777	4	BG972946	BG972946	602840675
	93	26	1.1	782	4	BG972529	BG972529	602841114
	94	26	1.1	788	2	BF781367	BF781367	602104549
	95	26	1.1	812	4	BG969879	BG969879	602838824
	96	26	1.1	875	2	BF788790	BF788790	602107191
	97	26	1.1	880	4	BI143297	BI143297	602907843
	98	26	1.1	886	4	BI101074	BI101074	602886333
	99	26	1.1	890	4	BI101705	BI101705	602887533
100	26	1.1	908	2	BF788011	BF788011	602113215	
101	26	1.1	910	4	BI099853	BI099853	602884666	
102	26	1.1	913	4	BG972966	BG972966	602840774	
103	26	1.1	956	2	BF784727	BF784727	602111365	
104	26	1.1	978	4	BI102968	BI102968	602888578	
105	26	1.1	1027	4	BG969791	BG969791	602838703	
106	26	1.1	1082	3	BC024453	BC024453	Mus muscu	
107	26	1.1	1185	9	AY404345	AY404345	Mus muscu	
108	26	1.1	1353	3	AK041045	AK041045	Mus muscu	
109	26	1.1	1452	2	BF782437	BF782437	602106145	
110	26	1.1	1723	3	AK052644	AK052644	Mus muscu	
111	26	1.1	2197	3	AK050128	AK050128	Mus muscu	
112	25	1.1	531	4	BI463768	BI463768	603203473	
c	113	24	1.0	549	9	CE651265	CE651265	tigr-gss-
c	114	24	1.0	718	6	CD634227	CD634227	56006276H
	115	23	1.0	556	2	BF080514	BF080514	231438 MA
	116	23	1.0	899	4	BI246549	BI246549	602958449
	117	23	1.0	965	2	BF789220	BF789220	602105115
c	118	22	0.9	435	6	CB793261	CB793261	AMGNNUC:M
c	119	22	0.9	447	1	AA176547	AA176547	zp37d04.r
c	120	22	0.9	487	9	CE422925	CE422925	tigr-gss-
c	121	22	0.9	494	8	AQ185578	AQ185578	HS_2241_A
c	122	22	0.9	544	4	BG679008	BG679008	602624931

123	22	0.9	580	9	CE054365	CE054365	tigr-gss-
124	22	0.9	602	4	BI693709	BI693709	603342026
c 125	22	0.9	603	9	CE843398	CE843398	tigr-gss-
c 126	22	0.9	606	9	CE149561	CE149561	tigr-gss-
c 127	22	0.9	631	7	CN306203	CN306203	328823352
c 128	22	0.9	675	2	BE378177	BE378177	601237924
c 129	22	0.9	695	1	AL110426	AL110426	DKFZp434L
130	22	0.9	751	6	CB952810	CB952810	AGENCOURT
131	22	0.9	763	6	CD241803	CD241803	AGENCOURT
c 132	22	0.9	766	5	BU281446	BU281446	603865111
133	22	0.9	769	9	CE543749	CE543749	tigr-gss-
c 134	22	0.9	841	2	BE378743	BE378743	601237186
c 135	22	0.9	894	4	BG747705	BG747705	602705178
c 136	21	0.9	124	8	BH104708	BH104708	RPCI-24-3
c 137	21	0.9	127	2	BF514925	BF514925	UI-H-BW1-
c 138	21	0.9	302	4	BG023045	BG023045	dab11a07.
139	21	0.9	407	6	CB434861	CB434861	611551 MA
c 140	21	0.9	461	4	BG438773	BG438773	dab28d12.
c 141	21	0.9	485	1	AA009868	AA009868	zi07d01.r
142	21	0.9	488	6	CB433209	CB433209	609534 MA
c 143	21	0.9	520	4	BI312811	BI312811	dai27c06.
144	21	0.9	538	8	AQ793538	AQ793538	HS_5269_A
c 145	21	0.9	552	4	BM179355	BM179355	dai42e11.
146	21	0.9	581	6	CA768818	CA768818	ssalbrh01
147	21	0.9	594	5	BU664018	BU664018	cl110b07.
c 148	21	0.9	598	5	BQ400420	BQ400420	NISC mp09
c 149	21	0.9	617	7	CN668302	CN668302	A0865D05-
150	21	0.9	644	6	CA047596	CA047596	ssalpit15
151	21	0.9	657	6	CA119273	CA119273	SCBGLR111
c 152	21	0.9	659	4	BI181339	BI181339	UNL-P-FN-
153	21	0.9	691	9	CE286860	CE286860	tigr-gss-
c 154	21	0.9	718	9	CR159413	CR159413	Reverse s
c 155	21	0.9	745	6	CD634233	CD634233	56006392H
156	21	0.9	835	9	CC577742	CC577742	CH240_456
157	21	0.9	946	9	CL028334	CL028334	CH216-27G
158	21	0.9	1003	9	CL021858	CL021858	CH216-8P2
159	21	0.9	1035	9	CL112702	CL112702	ISB1-57I8
160	21	0.9	1060	9	CL079312	CL079312	CH216-155
161	21	0.9	1154	9	CL048289	CL048289	CH216-67L
c 162	21	0.9	1229	9	CL641750	CL641750	CH213-17F
c 163	20	0.9	169	9	CE339517	CE339517	tigr-gss-
c 164	20	0.9	194	7	H90273	H90273	yu88h02.r1
c 165	20	0.9	244	9	CE376292	CE376292	tigr-gss-
166	20	0.9	262	9	CR037191	CR037191	Forward s
167	20	0.9	272	9	CR504199	CR504199	Medicago
c 168	20	0.9	306	8	AZ067600	AZ067600	RPCI-23-4
169	20	0.9	334	9	CE469814	CE469814	tigr-gss-
170	20	0.9	357	4	BM184978	BM184978	ft84h04.y
171	20	0.9	385	4	BI708244	BI708244	ft45a09.y
172	20	0.9	386	4	BM534166	BM534166	fw94e12.y
173	20	0.9	393	4	BM081091	BM081091	ft80c06.y
174	20	0.9	394	7	CO921569	CO921569	AGENCOURT
175	20	0.9	398	7	CO951549	CO951549	UMC-pd12f
c 176	20	0.9	409	7	CF796013	CF796013	892225 MA
c 177	20	0.9	417	9	CE656318	CE656318	tigr-gss-
178	20	0.9	419	6	CB799389	CB799389	AMGNNUC:N
c 179	20	0.9	423	5	BY153866	BY153866	BY153866

c 180	20	0.9	434	1	AA997348	AA997348	UI-R-C0-h
181	20	0.9	434	2	BB847184	BB847184	BB847184
182	20	0.9	436	1	AV590825	AV590825	AV590825
183	20	0.9	442	4	BG145555	BG145555	uu89f10.x
184	20	0.9	443	9	CE787473	CE787473	tigr-gss-
c 185	20	0.9	450	9	AG234986	AG234986	Lotus cor
186	20	0.9	452	7	CK869895	CK869895	AGENCOURT
c 187	20	0.9	459	2	BB774032	BB774032	BB774032
188	20	0.9	459	7	CN175733	CN175733	AGENCOURT
189	20	0.9	464	8	AQ199079	AQ199079	RPCI11-67
190	20	0.9	486	9	CE410827	CE410827	tigr-gss-
191	20	0.9	535	1	AL728282	AL728282	AL728282
192	20	0.9	535	7	CK485388	CK485388	rswab0_00
193	20	0.9	537	4	BM265868	BM265868	fw36h01.y
c 194	20	0.9	537	9	CE007131	CE007131	tigr-gss-
195	20	0.9	546	9	CE154600	CE154600	tigr-gss-
196	20	0.9	552	9	CE702878	CE702878	tigr-gss-
197	20	0.9	556	8	AZ898442	AZ898442	RPCI-24-1
c 198	20	0.9	558	9	CE182816	CE182816	tigr-gss-
c 199	20	0.9	570	8	AZ719183	AZ719183	RPCI-24-1
200	20	0.9	571	9	CE062973	CE062973	tigr-gss-
201	20	0.9	572	7	CK528088	CK528088	rswfa0_00
c 202	20	0.9	575	6	CB608077	CB608077	AMGNNUC:U
c 203	20	0.9	577	5	BX372905	BX372905	BX372905
204	20	0.9	581	7	CK683510	CK683510	ZF101-P00
205	20	0.9	587	9	CE523313	CE523313	tigr-gss-
206	20	0.9	594	8	AZ519016	AZ519016	RPCI-11-6
207	20	0.9	598	7	CK543959	CK543959	rswhb0_01
c 208	20	0.9	599	1	AL728365	AL728365	AL728365
c 209	20	0.9	599	9	CC876108	CC876108	ZMMBBb019
210	20	0.9	602	9	CC519891	CC519891	CH240_367
211	20	0.9	605	9	CE712865	CE712865	tigr-gss-
212	20	0.9	606	6	CB477435	CB477435	jns21_D12
c 213	20	0.9	606	9	CE561587	CE561587	tigr-gss-
214	20	0.9	607	8	B15910	B15910	346G22.TP C
215	20	0.9	609	9	CE109632	CE109632	tigr-gss-
216	20	0.9	613	9	CE230609	CE230609	tigr-gss-
c 217	20	0.9	615	7	CF944378	CF944378	TrEST-A01
c 218	20	0.9	617	9	CE632953	CE632953	tigr-gss-
c 219	20	0.9	627	9	CE574673	CE574673	tigr-gss-
c 220	20	0.9	631	4	BG380796	BG380796	UI-R-CT0-
c 221	20	0.9	636	9	CE596340	CE596340	tigr-gss-
222	20	0.9	646	7	CF176428	CF176428	800514 MA
c 223	20	0.9	651	8	AQ422848	AQ422848	CITBI-E1-
224	20	0.9	652	7	CK490418	CK490418	rswab0_00
225	20	0.9	659	8	AZ639923	AZ639923	1M0501I11
c 226	20	0.9	660	9	CE257388	CE257388	tigr-gss-
227	20	0.9	660	9	CE708420	CE708420	tigr-gss-
228	20	0.9	661	9	CE055128	CE055128	tigr-gss-
229	20	0.9	663	9	CE360895	CE360895	tigr-gss-
c 230	20	0.9	664	9	CE576178	CE576178	tigr-gss-
c 231	20	0.9	665	2	BB624520	BB624520	BB624520
c 232	20	0.9	666	9	AG576200	AG576200	Mus muscu
233	20	0.9	672	9	CE713784	CE713784	tigr-gss-
234	20	0.9	675	9	CE378054	CE378054	tigr-gss-
235	20	0.9	679	9	AG063221	AG063221	Pan trogl
c 236	20	0.9	684	9	CE530025	CE530025	tigr-gss-

c 237	20	0.9	685	8	AZ332140	AZ332140	1M0060P17
c 238	20	0.9	692	9	CE766558	CE766558	tigr-gss-
239	20	0.9	700	1	AL714811	AL714811	AL714811
c 240	20	0.9	703	1	AL723751	AL723751	AL723751
241	20	0.9	705	1	AL718833	AL718833	AL718833
c 242	20	0.9	707	1	AL714719	AL714719	AL714719
243	20	0.9	712	9	CE701121	CE701121	tigr-gss-
c 244	20	0.9	714	9	CE210749	CE210749	tigr-gss-
245	20	0.9	731	9	CE026066	CE026066	tigr-gss-
246	20	0.9	737	9	CE324466	CE324466	tigr-gss-
c 247	20	0.9	747	8	BZ138378	BZ138378	CH230-386
c 248	20	0.9	761	9	BX993602	BX993602	Forward s
c 249	20	0.9	767	1	AL721817	AL721817	AL721817
250	20	0.9	767	9	AG532581	AG532581	Mus muscu
251	20	0.9	772	7	CV483753	CV483753	AGENCOURT
c 252	20	0.9	772	9	CE553349	CE553349	tigr-gss-
c 253	20	0.9	778	9	CG135785	CG135785	PUFNI24TD
c 254	20	0.9	781	9	AG417163	AG417163	Mus muscu
255	20	0.9	791	9	CC524962	CC524962	CH240_399
c 256	20	0.9	794	9	CR205323	CR205323	Reverse s
257	20	0.9	797	9	AJ589546	AJ589546	Arabidops
c 258	20	0.9	802	9	CE041036	CE041036	tigr-gss-
c 259	20	0.9	806	9	BX155188	BX155188	Danio rer
c 260	20	0.9	810	9	CR111618	CR111618	Reverse s
261	20	0.9	821	9	CC491351	CC491351	CH240_325
c 262	20	0.9	849	4	BJ727786	BJ727786	BJ727786
263	20	0.9	853	2	AW054025	AW054025	L30-1884T
264	20	0.9	884	8	BH130649	BH130649	ENTOW41TF
c 265	20	0.9	889	6	CA491373	CA491373	AGENCOURT
266	20	0.9	894	9	CR102774	CR102774	Forward s
c 267	20	0.9	896	9	CNS05BTS	AL330265	Tetraodon
268	20	0.9	901	9	CR270966	CR270966	Forward s
269	20	0.9	938	9	CG135784	CG135784	PUFNI24TB
270	20	0.9	942	9	CL393323	CL393323	ZMMBBb019
271	20	0.9	1036	8	CC255743	CC255743	CH261-79E
c 272	20	0.9	1062	9	CNS05BUU	AL330303	Tetraodon
c 273	20	0.9	1107	4	BM548110	BM548110	AGENCOURT
274	20	0.9	1174	8	CC203459	CC203459	CH261-47I
c 275	20	0.9	1850	3	AK033339	AK033339	Mus muscu
c 276	20	0.9	4022	3	AK041687	AK041687	Mus muscu
c 277	19	0.8	47	9	CL214736	CL214736	M073D06 G
278	19	0.8	102	8	AZ248747	AZ248747	RPCI-23-4
279	19	0.8	104	2	AW709225	AW709225	d3g08ne.f
280	19	0.8	122	4	BG952052	BG952052	MR1-CT073
c 281	19	0.8	124	4	BG950878	BG950878	MR1-CT073
282	19	0.8	147	9	LBAF004H05	BX539790	Leishmani
c 283	19	0.8	159	8	AZ633044	AZ633044	1M0488I04
284	19	0.8	160	7	CO356090	CO356090	DR_ATE_NR
c 285	19	0.8	171	9	CE433379	CE433379	tigr-gss-
286	19	0.8	180	9	CE204377	CE204377	tigr-gss-
c 287	19	0.8	182	2	BE149929	BE149929	RC0-HT025
c 288	19	0.8	199	9	CE588538	CE588538	tigr-gss-
289	19	0.8	207	9	CE738101	CE738101	tigr-gss-
c 290	19	0.8	209	9	CNS02ECX	AL193578	Tetraodon
291	19	0.8	210	1	AJ282887	AJ282887	4A3A-P10F
292	19	0.8	211	2	BE149928	BE149928	RC0-HT025
c 293	19	0.8	213	9	CE067769	CE067769	tigr-gss-

	294	19	0.8	214	2	AW815495	AW815495	QV0-ST021
c	295	19	0.8	214	9	CE208799	CE208799	tigr-gss-
	296	19	0.8	214	9	CE726333	CE726333	tigr-gss-
c	297	19	0.8	215	9	CE414518	CE414518	tigr-gss-
	298	19	0.8	224	9	CE520482	CE520482	tigr-gss-
c	299	19	0.8	227	9	BX534851	BX534851	Arabidops
	300	19	0.8	229	8	BH655130	BH655130	BOHXI15TF
c	301	19	0.8	231	9	CE760820	CE760820	tigr-gss-
c	302	19	0.8	235	9	CE200414	CE200414	tigr-gss-
c	303	19	0.8	236	9	CE077168	CE077168	tigr-gss-
c	304	19	0.8	236	9	CE327796	CE327796	tigr-gss-
c	305	19	0.8	237	9	CE072544	CE072544	tigr-gss-
c	306	19	0.8	238	2	BB262215	BB262215	BB262215
c	307	19	0.8	239	5	BU386241	BU386241	603860930
c	308	19	0.8	242	9	CE539955	CE539955	tigr-gss-
	309	19	0.8	249	9	CE030499	CE030499	tigr-gss-
c	310	19	0.8	250	9	CE486471	CE486471	tigr-gss-
	311	19	0.8	251	9	CL449822	CL449822	ZMMBBb047
	312	19	0.8	252	9	CL959889	CL959889	OsIFCC036
	313	19	0.8	257	7	CK614293	CK614293	LPSe_D23
	314	19	0.8	259	9	CE627861	CE627861	tigr-gss-
	315	19	0.8	260	1	AV274662	AV274662	AV274662
c	316	19	0.8	262	7	F04518	F04518	HSCZPH012 n
c	317	19	0.8	263	1	AI094659	AI094659	oy61f01.s
c	318	19	0.8	264	1	AA296900	AA296900	EST112458
	319	19	0.8	265	6	CA950542	CA950542	ir90c01.y
c	320	19	0.8	268	2	BB466444	BB466444	BB466444
	321	19	0.8	269	9	CE018071	CE018071	tigr-gss-
	322	19	0.8	269	9	CE512239	CE512239	tigr-gss-
c	323	19	0.8	271	2	BB528131	BB528131	BB528131
c	324	19	0.8	272	9	CE324366	CE324366	tigr-gss-
	325	19	0.8	274	9	CE538693	CE538693	tigr-gss-
c	326	19	0.8	277	1	AV217821	AV217821	AV217821
	327	19	0.8	277	9	CE266163	CE266163	tigr-gss-
c	328	19	0.8	280	9	CE653527	CE653527	tigr-gss-
	329	19	0.8	284	9	CE710156	CE710156	tigr-gss-
c	330	19	0.8	285	6	CF032947	CF032947	QCF10cl2.
c	331	19	0.8	285	9	CE632956	CE632956	tigr-gss-
c	332	19	0.8	286	9	CE484767	CE484767	tigr-gss-
c	333	19	0.8	287	2	BB191017	BB191017	BB191017
c	334	19	0.8	287	9	CE539872	CE539872	tigr-gss-
c	335	19	0.8	289	2	BB267346	BB267346	BB267346
c	336	19	0.8	289	6	CD152000	CD152000	ML1-0027T
c	337	19	0.8	291	9	CE182081	CE182081	tigr-gss-
	338	19	0.8	292	9	CE028288	CE028288	tigr-gss-
c	339	19	0.8	293	2	BB264514	BB264514	BB264514
c	340	19	0.8	294	7	CN351899	CN351899	170005328
c	341	19	0.8	294	9	CE543781	CE543781	tigr-gss-
c	342	19	0.8	296	6	CD612735	CD612735	56029315J
	343	19	0.8	297	9	CE420939	CE420939	tigr-gss-
	344	19	0.8	298	9	CG914090	CG914090	ZMMBBb037
	345	19	0.8	299	2	AW713801	AW713801	h2g11ne.f
	346	19	0.8	299	6	CD612734	CD612734	56029315H
c	347	19	0.8	300	9	BX004009	BX004009	Arabidops
	348	19	0.8	304	9	CE575398	CE575398	tigr-gss-
c	349	19	0.8	307	1	AI435198	AI435198	tilla01.x
c	350	19	0.8	307	9	CE454878	CE454878	tigr-gss-

	351	19	0.8	307	9	CE483853	CE483853	tigr-gss-
	352	19	0.8	309	9	CE370950	CE370950	tigr-gss-
c	353	19	0.8	310	2	BB103174	BB103174	BB103174
	354	19	0.8	315	9	CE164303	CE164303	tigr-gss-
c	355	19	0.8	315	9	CE570748	CE570748	tigr-gss-
c	356	19	0.8	316	9	CE106984	CE106984	tigr-gss-
	357	19	0.8	316	9	CE408328	CE408328	tigr-gss-
c	358	19	0.8	316	9	CE732166	CE732166	tigr-gss-
c	359	19	0.8	317	9	BX660820	BX660820	Arabidops
	360	19	0.8	318	4	BI800097	BI800097	H147F08 E
c	361	19	0.8	319	7	T24109	T24109	seq2297 Cot
c	362	19	0.8	321	8	AZ564000	AZ564000	RPCI-23-2
c	363	19	0.8	321	9	CE016313	CE016313	tigr-gss-
c	364	19	0.8	323	1	AV683895	AV683895	AV683895
c	365	19	0.8	323	9	CE204559	CE204559	tigr-gss-
c	366	19	0.8	324	1	AI886619	AI886619	tz59h04.x
	367	19	0.8	324	9	CL980220	CL980220	OsIFCC034
	368	19	0.8	325	6	CD959714	CD959714	SCY_111 G
c	369	19	0.8	326	5	BY110280	BY110280	BY110280
	370	19	0.8	326	7	CV165679	CV165679	rsmsxl_00
	371	19	0.8	326	9	CE308758	CE308758	tigr-gss-
c	372	19	0.8	327	5	BY107492	BY107492	BY107492
c	373	19	0.8	329	2	BE711259	BE711259	RC6-HT067
c	374	19	0.8	329	5	BY110750	BY110750	BY110750
c	375	19	0.8	331	9	CE523580	CE523580	tigr-gss-
	376	19	0.8	335	9	CE033215	CE033215	tigr-gss-
	377	19	0.8	338	9	CE564098	CE564098	tigr-gss-
	378	19	0.8	339	9	CE591396	CE591396	tigr-gss-
	379	19	0.8	340	5	BU853917	BU853917	AGENCOURT
c	380	19	0.8	342	9	CE238041	CE238041	tigr-gss-
	381	19	0.8	343	2	AW480786	AW480786	33285 MAR
c	382	19	0.8	347	9	CE796067	CE796067	tigr-gss-
	383	19	0.8	350	9	CE096783	CE096783	tigr-gss-
	384	19	0.8	357	9	CE443622	CE443622	tigr-gss-
c	385	19	0.8	358	9	CE582615	CE582615	tigr-gss-
c	386	19	0.8	359	1	AI522340	AI522340	fb18e12.x
	387	19	0.8	359	2	BE415737	BE415737	MWL039.B0
	388	19	0.8	359	9	CE351850	CE351850	tigr-gss-
	389	19	0.8	360	9	CE732059	CE732059	tigr-gss-
c	390	19	0.8	362	8	BZ133937	BZ133937	CH230-385
c	391	19	0.8	363	9	CE163338	CE163338	tigr-gss-
c	392	19	0.8	364	7	CK764274	CK764274	pam01-13m
	393	19	0.8	364	9	CE690486	CE690486	tigr-gss-
	394	19	0.8	366	9	CE172310	CE172310	tigr-gss-
	395	19	0.8	368	9	CE805087	CE805087	tigr-gss-
c	396	19	0.8	370	9	CE216693	CE216693	tigr-gss-
c	397	19	0.8	371	2	AW674454	AW674454	ba63c01.x
c	398	19	0.8	371	9	CE125478	CE125478	tigr-gss-
	399	19	0.8	372	9	CE429239	CE429239	tigr-gss-
	400	19	0.8	373	9	CE723064	CE723064	tigr-gss-
	401	19	0.8	374	9	CE041628	CE041628	tigr-gss-
	402	19	0.8	374	9	CE524318	CE524318	tigr-gss-
c	403	19	0.8	376	1	AI734930	AI734930	atl4d05.x
c	404	19	0.8	376	7	CF230525	CF230525	PtaC0009D
	405	19	0.8	377	9	CE694673	CE694673	tigr-gss-
c	406	19	0.8	380	9	CE308274	CE308274	tigr-gss-
c	407	19	0.8	381	9	CE658419	CE658419	tigr-gss-

	408	19	0.8	382	9	CE466702	CE466702	tigr-gss-
c	409	19	0.8	382	9	CE487403	CE487403	tigr-gss-
	410	19	0.8	383	4	BI131705	BI131705	G124P56Y
	411	19	0.8	383	5	BY006002	BY006002	BY006002
	412	19	0.8	384	8	AQ807226	AQ807226	HS_3127_B
c	413	19	0.8	384	8	AQ580886	AQ580886	RPCI-11-4
c	414	19	0.8	386	9	CE743865	CE743865	tigr-gss-
	415	19	0.8	388	2	AW434729	AW434729	UI-R-BJ0p
	416	19	0.8	389	1	AA397322	AA397322	mr40b11.r
c	417	19	0.8	390	9	CE194014	CE194014	tigr-gss-
c	418	19	0.8	391	5	BP650827	BP650827	BP650827
c	419	19	0.8	391	9	CE263871	CE263871	tigr-gss-
c	420	19	0.8	392	6	CB774799	CB774799	AMGNNUC:S
	421	19	0.8	393	9	CE159307	CE159307	tigr-gss-
	422	19	0.8	393	9	CE275945	CE275945	tigr-gss-
c	423	19	0.8	395	9	CE388438	CE388438	tigr-gss-
c	424	19	0.8	396	4	BG883353	BG883353	fp26f01.x
c	425	19	0.8	396	7	CF231111	CF231111	PtaC0017E
c	426	19	0.8	397	9	CE171641	CE171641	tigr-gss-
c	427	19	0.8	398	8	AQ145732	AQ145732	HS_2216_A
	428	19	0.8	399	9	CE440871	CE440871	tigr-gss-
	429	19	0.8	400	9	CE310652	CE310652	tigr-gss-
	430	19	0.8	402	9	CE248134	CE248134	tigr-gss-
	431	19	0.8	402	9	CE596949	CE596949	tigr-gss-
c	432	19	0.8	404	9	CC795797	CC795797	SALK_0883
	433	19	0.8	405	6	CD407923	CD407923	Gm_ck3369
	434	19	0.8	407	9	CE280199	CE280199	tigr-gss-
c	435	19	0.8	410	2	BE172984	BE172984	MR0-HT055
c	436	19	0.8	410	7	R14675	R14675	yf92b05.rl
c	437	19	0.8	410	9	CE785393	CE785393	tigr-gss-
	438	19	0.8	412	9	AL768945	AL768945	Arabidops
	439	19	0.8	412	9	CC958229	CC958229	BOICX65TR
c	440	19	0.8	413	4	BI129781	BI129781	G095P54Y
c	441	19	0.8	413	8	AQ435710	AQ435710	HS_5148_B
	442	19	0.8	415	6	CB800643	CB800643	AMGNNUC:S
	443	19	0.8	416	5	BY246714	BY246714	BY246714
c	444	19	0.8	416	9	CE762505	CE762505	tigr-gss-
	445	19	0.8	419	8	BZ913278	BZ913278	CH240_53P
	446	19	0.8	421	2	BB704505	BB704505	BB704505
	447	19	0.8	421	8	BZ384590	BZ384590	SALK_1357
c	448	19	0.8	422	9	CE742419	CE742419	tigr-gss-
c	449	19	0.8	424	8	BZ415985	BZ415985	if61h03.g
c	450	19	0.8	426	8	AZ151834	AZ151834	SP_0038_B
c	451	19	0.8	427	9	CE053127	CE053127	tigr-gss-
	452	19	0.8	427	9	CE651624	CE651624	tigr-gss-
c	453	19	0.8	428	7	N24605	N24605	yx72e05.sl
	454	19	0.8	429	1	AA797863	AA797863	vw31g10.r
	455	19	0.8	429	5	BY180909	BY180909	BY180909
	456	19	0.8	429	8	BZ943150	BZ943150	CH240_80H
	457	19	0.8	429	8	AQ636784	AQ636784	RPCI-11-4
c	458	19	0.8	429	9	CE054838	CE054838	tigr-gss-
	459	19	0.8	431	9	CE022381	CE022381	tigr-gss-
c	460	19	0.8	431	9	CE168437	CE168437	tigr-gss-
c	461	19	0.8	431	9	CE401510	CE401510	tigr-gss-
c	462	19	0.8	431	9	CG398567	CG398567	ZMMBBc001
	463	19	0.8	433	5	BY283433	BY283433	BY283433
c	464	19	0.8	434	9	AG195209	AG195209	Pan trogl

c 465	19	0.8	435	6	BY532671	BY532671	BY532671
c 466	19	0.8	435	6	CA799585	CA799585	sat35h11.
c 467	19	0.8	435	8	BH749116	BH749116	SALK_0473
c 468	19	0.8	435	9	CE418826	CE418826	tigr-gss-
469	19	0.8	435	9	CE632990	CE632990	tigr-gss-
c 470	19	0.8	436	2	AW228656	AW228656	up15h09.x
c 471	19	0.8	436	2	BE350286	BE350286	ht12f08.x
c 472	19	0.8	436	4	BI293355	BI293355	UI-R-DK0-
c 473	19	0.8	436	9	CE812891	CE812891	tigr-gss-
474	19	0.8	438	9	CE246842	CE246842	tigr-gss-
c 475	19	0.8	439	7	CN399825	CN399825	170004243
476	19	0.8	439	9	CE532786	CE532786	tigr-gss-
c 477	19	0.8	442	7	CN967657	CN967657	15154_100
478	19	0.8	442	9	CE082046	CE082046	tigr-gss-
c 479	19	0.8	442	9	CE643112	CE643112	tigr-gss-
c 480	19	0.8	444	1	AV723736	AV723736	AV723736
c 481	19	0.8	446	8	AQ154983	AQ154983	HS_3037_A
482	19	0.8	448	9	CE783536	CE783536	tigr-gss-
483	19	0.8	449	1	AL828300	AL828300	AL828300
c 484	19	0.8	449	6	CD555738	CD555738	B0397B11-
c 485	19	0.8	449	9	CE675203	CE675203	tigr-gss-
486	19	0.8	450	8	AQ027077	AQ027077	CIT-HSP-2
c 487	19	0.8	450	9	CE699613	CE699613	tigr-gss-
c 488	19	0.8	451	9	CE084498	CE084498	tigr-gss-
c 489	19	0.8	452	2	BF887837	BF887837	QV2-TN017
490	19	0.8	452	2	BB839850	BB839850	BB839850
c 491	19	0.8	452	2	BE335337	BE335337	ug98d07.x
492	19	0.8	452	6	CD159837	CD159837	ML1-0064P
c 493	19	0.8	452	9	CE678493	CE678493	tigr-gss-
c 494	19	0.8	453	8	AZ419750	AZ419750	1M0196I13
495	19	0.8	453	8	AQ208915	AQ208915	HS_3230_A
496	19	0.8	454	5	BY252260	BY252260	BY252260
497	19	0.8	454	9	CE242539	CE242539	tigr-gss-
c 498	19	0.8	455	2	BF711381	BF711381	MI-P-A1-a
499	19	0.8	455	5	BY239481	BY239481	BY239481
500	19	0.8	456	4	BG012069	BG012069	RC3-GN027
c 501	19	0.8	457	2	BF706341	BF706341	280656 MA
502	19	0.8	457	4	BI060835	BI060835	IL3-UT011
c 503	19	0.8	457	9	CE316095	CE316095	tigr-gss-
504	19	0.8	458	4	BI060832	BI060832	IL3-UT011
505	19	0.8	458	7	N62141	N62141	yz62b07.s1
c 506	19	0.8	459	8	BH327848	BH327848	CH230-450
507	19	0.8	461	9	CE659288	CE659288	tigr-gss-
c 508	19	0.8	462	8	BZ198526	BZ198526	CH230-322
509	19	0.8	463	9	CE208987	CE208987	tigr-gss-
c 510	19	0.8	463	9	CE415203	CE415203	tigr-gss-
511	19	0.8	463	9	CE622682	CE622682	tigr-gss-
512	19	0.8	465	2	AW710350	AW710350	e3b03ne.f
c 513	19	0.8	466	8	AZ419439	AZ419439	1M0195O23
c 514	19	0.8	467	8	CC168193	CC168193	ij83a08.b
515	19	0.8	468	6	CD740207	CD740207	4029011 1
516	19	0.8	468	8	AZ845709	AZ845709	2M0145D12
c 517	19	0.8	468	8	BZ187606	BZ187606	CH230-435
518	19	0.8	469	6	CD878973	CD878973	AZO4.104A
c 519	19	0.8	469	7	H44410	H44410	yo74d04.s1
520	19	0.8	470	2	BE848382	BE848382	uw37h11.y
c 521	19	0.8	470	9	CE398868	CE398868	tigr-gss-

c	522	19	0.8	470	9	CE403345	CE403345	tigr-gss-
c	523	19	0.8	471	9	CE701710	CE701710	tigr-gss-
	524	19	0.8	472	4	BG148767	BG148767	uu81a02.y
c	525	19	0.8	472	9	CE717772	CE717772	tigr-gss-
	526	19	0.8	473	6	CD160420	CD160420	ML1-0066G
	527	19	0.8	473	8	BH030764	BH030764	RPCI-24-2
c	528	19	0.8	473	9	CE601638	CE601638	tigr-gss-
	529	19	0.8	475	8	AQ616676	AQ616676	HS_5153_A
	530	19	0.8	476	4	BG383826	BG383826	302221_MA
	531	19	0.8	476	9	CE279300	CE279300	tigr-gss-
	532	19	0.8	477	8	AZ889580	AZ889580	RPCI-24-1
	533	19	0.8	479	9	CE013496	CE013496	tigr-gss-
c	534	19	0.8	481	8	BZ311544	BZ311544	ic69c07.b
	535	19	0.8	481	9	CE053817	CE053817	tigr-gss-
	536	19	0.8	482	9	CE653044	CE653044	tigr-gss-
	537	19	0.8	482	9	CE769211	CE769211	tigr-gss-
c	538	19	0.8	483	6	CD297498	CD297498	StrPu691.
c	539	19	0.8	483	7	CK555864	CK555864	rswla0_02
	540	19	0.8	484	9	CE408225	CE408225	tigr-gss-
	541	19	0.8	485	8	BH776532	BH776532	fzmb013f0
	542	19	0.8	486	9	CE122510	CE122510	tigr-gss-
c	543	19	0.8	486	9	CE613461	CE613461	tigr-gss-
c	544	19	0.8	487	7	CN679395	CN679395	E0123H09-
c	545	19	0.8	487	8	BZ159296	BZ159296	CH230-289
	546	19	0.8	488	6	CA656546	CA656546	wlm0.pk00
	547	19	0.8	488	7	CN792544	CN792544	4127418_B
	548	19	0.8	491	9	CE110968	CE110968	tigr-gss-
	549	19	0.8	491	9	CE347474	CE347474	tigr-gss-
	550	19	0.8	493	8	AZ891386	AZ891386	RPCI-24-1
	551	19	0.8	493	9	CE060627	CE060627	tigr-gss-
	552	19	0.8	493	9	CE717097	CE717097	tigr-gss-
	553	19	0.8	494	9	CE649507	CE649507	tigr-gss-
c	554	19	0.8	495	9	CE265505	CE265505	tigr-gss-
	555	19	0.8	496	9	CE087107	CE087107	tigr-gss-
c	556	19	0.8	496	9	CE374119	CE374119	tigr-gss-
c	557	19	0.8	496	9	CE806116	CE806116	tigr-gss-
c	558	19	0.8	497	5	BU738882	BU738882	UI-E-EJ0-
	559	19	0.8	497	9	CE012709	CE012709	tigr-gss-
	560	19	0.8	497	9	CE068561	CE068561	tigr-gss-
	561	19	0.8	498	7	CK738707	CK738707	OF04F03-T
c	562	19	0.8	498	9	CE094979	CE094979	tigr-gss-
c	563	19	0.8	501	9	CE188918	CE188918	tigr-gss-
	564	19	0.8	501	9	CE750586	CE750586	tigr-gss-
	565	19	0.8	502	5	BX921161	BX921161	BX921161
	566	19	0.8	502	6	CD150391	CD150391	ML1-0020T
c	567	19	0.8	502	7	R43640	R43640	yg20q08.s1
c	568	19	0.8	502	9	CE619628	CE619628	tigr-gss-
c	569	19	0.8	502	9	CE640383	CE640383	tigr-gss-
	570	19	0.8	503	9	CE331433	CE331433	tigr-gss-
	571	19	0.8	503	9	CE413671	CE413671	tigr-gss-
	572	19	0.8	504	9	CE588004	CE588004	tigr-gss-
	573	19	0.8	505	2	BE040658	BE040658	OF04F03_O
	574	19	0.8	505	4	BG467088	BG467088	1A04D04_B
	575	19	0.8	505	9	CE505312	CE505312	tigr-gss-
	576	19	0.8	505	9	CE787301	CE787301	tigr-gss-
c	577	19	0.8	506	6	CD096095	CD096095	ME1-0006T
	578	19	0.8	506	7	CV162940	CV162940	rsmsxl_00

c 579	19	0.8	506	9	CE729747	CE729747 tigr-gss-
580	19	0.8	507	9	CE292269	CE292269 tigr-gss-
581	19	0.8	510	4	BG263863	BG263863 WHE2338_H
c 582	19	0.8	510	8	AQ625249	AQ625249 CITBI-E1-
c 583	19	0.8	510	9	CE476530	CE476530 tigr-gss-
584	19	0.8	512	5	BY248575	BY248575 BY248575
c 585	19	0.8	512	7	R59128	R59128 yg96b12.s1
586	19	0.8	512	9	CE279895	CE279895 tigr-gss-
587	19	0.8	514	4	BI127207	BI127207 G004P63Y
588	19	0.8	514	9	CE549647	CE549647 tigr-gss-
589	19	0.8	514	9	CE552711	CE552711 tigr-gss-
590	19	0.8	514	9	CE839568	CE839568 tigr-gss-
c 591	19	0.8	515	6	CB164148	CB164148 K-EST0225
c 592	19	0.8	515	8	BZ723789	BZ723789 PUCFG90TD
593	19	0.8	515	9	CE538885	CE538885 tigr-gss-
594	19	0.8	517	6	CA546327	CA546327 K0129E03-
c 595	19	0.8	518	5	BX102827	BX102827 BX102827
596	19	0.8	518	6	CA662859	CA662859 wlmk1.pk0
c 597	19	0.8	521	6	CB482157	CB482157 jns87_G12
c 598	19	0.8	521	9	CE733391	CE733391 tigr-gss-
599	19	0.8	522	9	CC943643	CC943643 BOICC06TR
600	19	0.8	522	9	CE059764	CE059764 tigr-gss-
601	19	0.8	524	2	BE429494	BE429494 TAS000.G0
c 602	19	0.8	525	8	AQ388687	AQ388687 RPCI11-15
c 603	19	0.8	525	9	CE403020	CE403020 tigr-gss-
604	19	0.8	527	9	CE490696	CE490696 tigr-gss-
c 605	19	0.8	527	9	CE613173	CE613173 tigr-gss-
c 606	19	0.8	528	9	CE482497	CE482497 tigr-gss-
607	19	0.8	529	6	CB555240	CB555240 MMSP0079_
608	19	0.8	529	9	CE487945	CE487945 tigr-gss-
609	19	0.8	530	4	BG226743	BG226743 kp93a04.y
610	19	0.8	530	9	CE541514	CE541514 tigr-gss-
611	19	0.8	531	7	CK680830	CK680830 ZF101-P00
612	19	0.8	531	9	CE219792	CE219792 tigr-gss-
613	19	0.8	531	9	CE717244	CE717244 tigr-gss-
c 614	19	0.8	532	9	CE007968	CE007968 tigr-gss-
c 615	19	0.8	532	9	CE597285	CE597285 tigr-gss-
616	19	0.8	532	9	CE626023	CE626023 tigr-gss-
617	19	0.8	534	7	CF303787	CF303787 ABF1--03-
618	19	0.8	536	9	CE124294	CE124294 tigr-gss-
c 619	19	0.8	537	9	CE463095	CE463095 tigr-gss-
c 620	19	0.8	537	9	CE633358	CE633358 tigr-gss-
621	19	0.8	538	9	CE247788	CE247788 tigr-gss-
622	19	0.8	539	2	AW239732	AW239732 ptilc.pk0
623	19	0.8	539	9	CE175029	CE175029 tigr-gss-
c 624	19	0.8	540	2	AW189966	AW189966 xl10g04.x
625	19	0.8	541	2	BE031534	BE031534 130138 MA
626	19	0.8	541	7	CN231669	CN231669 WLB043E11
627	19	0.8	542	8	AZ274374	AZ274374 RPCI-23-1
c 628	19	0.8	542	9	CL372046	CL372046 RPCI44_30
629	19	0.8	543	5	BP165805	BP165805 BP165805
c 630	19	0.8	543	6	CD095982	CD095982 ME1-0006T
631	19	0.8	544	9	CE509611	CE509611 tigr-gss-
c 632	19	0.8	544	9	CE527528	CE527528 tigr-gss-
633	19	0.8	545	9	CE297785	CE297785 tigr-gss-
634	19	0.8	546	4	BF991122	BF991122 MR1-GN017
635	19	0.8	547	7	CK332163	CK332163 H8192C04-

	636	19	0.8	547	9	CE161422	CE161422	tigr-gss-
	637	19	0.8	547	9	CE172064	CE172064	tigr-gss-
c	638	19	0.8	547	9	CE331107	CE331107	tigr-gss-
c	639	19	0.8	548	9	CE030234	CE030234	tigr-gss-
	640	19	0.8	548	9	CE553198	CE553198	tigr-gss-
	641	19	0.8	548	9	CE575934	CE575934	tigr-gss-
c	642	19	0.8	548	9	CE715396	CE715396	tigr-gss-
	643	19	0.8	549	6	CF039804	CF039804	QCH4e10.y
c	644	19	0.8	549	9	CE036126	CE036126	tigr-gss-
c	645	19	0.8	550	9	CE099811	CE099811	tigr-gss-
c	646	19	0.8	551	9	CE412962	CE412962	tigr-gss-
	647	19	0.8	551	9	CE448884	CE448884	tigr-gss-
	648	19	0.8	552	9	CE313032	CE313032	tigr-gss-
	649	19	0.8	552	9	CE346760	CE346760	tigr-gss-
c	650	19	0.8	552	9	CE706206	CE706206	tigr-gss-
	651	19	0.8	553	9	BX239149	BX239149	Danio rer
	652	19	0.8	553	9	CE631870	CE631870	tigr-gss-
c	653	19	0.8	554	9	CL414099	CL414099	RPCI44_43
c	654	19	0.8	555	2	AW975322	AW975322	EST387430
c	655	19	0.8	555	4	BG352898	BG352898	sab92g05.
	656	19	0.8	555	9	CE123576	CE123576	tigr-gss-
	657	19	0.8	556	9	CE037936	CE037936	tigr-gss-
	658	19	0.8	556	9	CE462431	CE462431	tigr-gss-
	659	19	0.8	556	9	CE657014	CE657014	tigr-gss-
	660	19	0.8	557	9	CE812347	CE812347	tigr-gss-
	661	19	0.8	558	9	CE112077	CE112077	tigr-gss-
	662	19	0.8	558	9	CE113282	CE113282	tigr-gss-
c	663	19	0.8	558	9	CE259404	CE259404	tigr-gss-
	664	19	0.8	558	9	CE555033	CE555033	tigr-gss-
	665	19	0.8	558	9	CE627220	CE627220	tigr-gss-
	666	19	0.8	559	7	CN291419	CN291419	170006000
	667	19	0.8	559	9	CE575016	CE575016	tigr-gss-
	668	19	0.8	559	9	CE718853	CE718853	tigr-gss-
c	669	19	0.8	560	7	CF230998	CF230998	PtaC0016B
	670	19	0.8	560	8	BZ718661	BZ718661	PUCFF22TD
	671	19	0.8	560	9	CE561295	CE561295	tigr-gss-
c	672	19	0.8	561	5	BX351016	BX351016	BX351016
c	673	19	0.8	562	9	CE498349	CE498349	tigr-gss-
	674	19	0.8	562	9	CE561160	CE561160	tigr-gss-
c	675	19	0.8	563	8	AQ510431	AQ510431	nbxb0095M
	676	19	0.8	563	9	CE371029	CE371029	tigr-gss-
c	677	19	0.8	564	9	CE040030	CE040030	tigr-gss-
c	678	19	0.8	565	5	BU610740	BU610740	UI-M-FC0-
c	679	19	0.8	565	6	CD095805	CD095805	ME1-0006T
c	680	19	0.8	565	8	AZ601443	AZ601443	1M0419P09
	681	19	0.8	565	9	CE684214	CE684214	tigr-gss-
	682	19	0.8	566	8	BH327339	BH327339	CH230-105
	683	19	0.8	566	9	CE043674	CE043674	tigr-gss-
c	684	19	0.8	568	9	CE043736	CE043736	tigr-gss-
	685	19	0.8	568	9	CE143254	CE143254	tigr-gss-
c	686	19	0.8	568	9	CE649747	CE649747	tigr-gss-
	687	19	0.8	568	9	CE812360	CE812360	tigr-gss-
c	688	19	0.8	569	9	CE352673	CE352673	tigr-gss-
	689	19	0.8	569	9	CE543510	CE543510	tigr-gss-
	690	19	0.8	569	9	CE636208	CE636208	tigr-gss-
c	691	19	0.8	570	7	CF611501	CF611501	Lr_Cd2CF_
c	692	19	0.8	571	7	CF571043	CF571043	MCS008H09

693	19	0.8	571	9	CE816035	CE816035	tigr-gss-
694	19	0.8	572	6	CA733078	CA733078	wlplc.pk0
695	19	0.8	572	9	CE359182	CE359182	tigr-gss-
696	19	0.8	573	9	CE206234	CE206234	tigr-gss-
c 697	19	0.8	573	9	CE257376	CE257376	tigr-gss-
c 698	19	0.8	573	9	CE444590	CE444590	tigr-gss-
699	19	0.8	576	9	CE242973	CE242973	tigr-gss-
700	19	0.8	577	9	CE313890	CE313890	tigr-gss-
701	19	0.8	577	9	CE408304	CE408304	tigr-gss-
702	19	0.8	577	9	CE600265	CE600265	tigr-gss-
c 703	19	0.8	577	9	CE620115	CE620115	tigr-gss-
704	19	0.8	578	6	CA929693	CA929693	MTU2CA.P1
705	19	0.8	578	9	CE324758	CE324758	tigr-gss-
706	19	0.8	579	9	CE096313	CE096313	tigr-gss-
707	19	0.8	580	9	CE283406	CE283406	tigr-gss-
708	19	0.8	580	9	CE391770	CE391770	tigr-gss-
c 709	19	0.8	580	9	CE694128	CE694128	tigr-gss-
c 710	19	0.8	581	6	CB586906	CB586906	AMGNNUC:N
c 711	19	0.8	582	5	BQ537054	BQ537054	STEM2_19
c 712	19	0.8	582	9	CE291831	CE291831	tigr-gss-
c 713	19	0.8	582	9	CE653526	CE653526	tigr-gss-
c 714	19	0.8	582	9	CE823136	CE823136	tigr-gss-
c 715	19	0.8	583	9	CE677489	CE677489	tigr-gss-
716	19	0.8	583	9	CE787283	CE787283	tigr-gss-
717	19	0.8	583	9	CE853194	CE853194	tigr-gss-
c 718	19	0.8	584	8	AZ352712	AZ352712	1M0091K16
719	19	0.8	584	9	CE064780	CE064780	tigr-gss-
720	19	0.8	584	9	CE367487	CE367487	tigr-gss-
721	19	0.8	585	7	CF354804	CF354804	lac18e03.
c 722	19	0.8	585	8	BZ516376	BZ516376	BOMQT40TF
723	19	0.8	585	9	CE086408	CE086408	tigr-gss-
724	19	0.8	585	9	CE105967	CE105967	tigr-gss-
c 725	19	0.8	585	9	CE196653	CE196653	tigr-gss-
c 726	19	0.8	586	9	CE146890	CE146890	tigr-gss-
727	19	0.8	586	9	CE411571	CE411571	tigr-gss-
c 728	19	0.8	587	1	AJ658082	AJ658082	AJ658082
729	19	0.8	588	5	BU372677	BU372677	603590261
c 730	19	0.8	588	9	CE529559	CE529559	tigr-gss-
731	19	0.8	589	5	BQ116446	BQ116446	EST602022
732	19	0.8	589	9	CE113227	CE113227	tigr-gss-
c 733	19	0.8	589	9	CE524897	CE524897	tigr-gss-
734	19	0.8	590	7	CF111951	CF111951	Shultzomi
735	19	0.8	591	9	CE193352	CE193352	tigr-gss-
c 736	19	0.8	592	9	CE291854	CE291854	tigr-gss-
737	19	0.8	592	9	CE478157	CE478157	tigr-gss-
738	19	0.8	593	5	BQ553158	BQ553158	H4020D04-
739	19	0.8	593	9	CR478931	CR478931	Medicago
740	19	0.8	594	9	CE013914	CE013914	tigr-gss-
c 741	19	0.8	594	9	CE203000	CE203000	tigr-gss-
c 742	19	0.8	596	4	BI710340	BI710340	fq35a02.x
c 743	19	0.8	596	5	BX502501	BX502501	DKFZp779G
c 744	19	0.8	596	8	AQ637709	AQ637709	RPCI-11-4
c 745	19	0.8	596	9	CE116099	CE116099	tigr-gss-
746	19	0.8	596	9	CE298935	CE298935	tigr-gss-
747	19	0.8	596	9	CE379735	CE379735	tigr-gss-
748	19	0.8	596	9	CE653623	CE653623	tigr-gss-
749	19	0.8	596	9	CE827628	CE827628	tigr-gss-

	750	19	0.8	597	1	AL725528	AL725528	AL725528
	751	19	0.8	597	6	CB455366	CB455366	712504 MA
	752	19	0.8	597	9	CE222134	CE222134	tigr-gss-
	753	19	0.8	598	6	CA726716	CA726716	wdelf.pk0
	754	19	0.8	598	6	CD217981	CD217981	pgrln.pk0
	755	19	0.8	598	9	CE334679	CE334679	tigr-gss-
c	756	19	0.8	598	9	CE444235	CE444235	tigr-gss-
	757	19	0.8	598	9	CE544529	CE544529	tigr-gss-
c	758	19	0.8	598	9	CE558372	CE558372	tigr-gss-
	759	19	0.8	598	9	CE809529	CE809529	tigr-gss-
c	760	19	0.8	600	5	BX327664	BX327664	BX327664
c	761	19	0.8	600	9	CE713589	CE713589	tigr-gss-
	762	19	0.8	601	9	CE078569	CE078569	tigr-gss-
	763	19	0.8	601	9	CE155131	CE155131	tigr-gss-
c	764	19	0.8	602	9	CE511272	CE511272	tigr-gss-
	765	19	0.8	603	4	BM487089	BM487089	pgm2n.pk0
c	766	19	0.8	603	9	CE564159	CE564159	tigr-gss-
	767	19	0.8	604	9	CE467854	CE467854	tigr-gss-
c	768	19	0.8	604	9	CE490884	CE490884	tigr-gss-
	769	19	0.8	604	9	CE533046	CE533046	tigr-gss-
c	770	19	0.8	605	9	CE005744	CE005744	tigr-gss-
	771	19	0.8	605	9	CE012459	CE012459	tigr-gss-
c	772	19	0.8	605	9	CE352503	CE352503	tigr-gss-
	773	19	0.8	606	8	BZ934083	BZ934083	CH240_89D
	774	19	0.8	606	9	CE409770	CE409770	tigr-gss-
	775	19	0.8	606	9	CE811508	CE811508	tigr-gss-
	776	19	0.8	607	9	CE785124	CE785124	tigr-gss-
	777	19	0.8	608	9	CE344087	CE344087	tigr-gss-
c	778	19	0.8	608	9	CE530810	CE530810	tigr-gss-
c	779	19	0.8	609	7	CF229247	CF229247	PtaXM0023
c	780	19	0.8	609	9	CE193971	CE193971	tigr-gss-
	781	19	0.8	609	9	CE270700	CE270700	tigr-gss-
	782	19	0.8	609	9	CE563973	CE563973	tigr-gss-
	783	19	0.8	610	9	CE215895	CE215895	tigr-gss-
	784	19	0.8	610	9	CE336647	CE336647	tigr-gss-
	785	19	0.8	610	9	CE703958	CE703958	tigr-gss-
c	786	19	0.8	611	8	BH086863	BH086863	RPCI-24-3
	787	19	0.8	611	9	CR296869	CR296869	Medicago
	788	19	0.8	611	9	CE060580	CE060580	tigr-gss-
c	789	19	0.8	611	9	CE404589	CE404589	tigr-gss-
c	790	19	0.8	611	9	CE502525	CE502525	tigr-gss-
c	791	19	0.8	611	9	CE723162	CE723162	tigr-gss-
	792	19	0.8	612	9	CE154696	CE154696	tigr-gss-
c	793	19	0.8	612	9	CE333461	CE333461	tigr-gss-
	794	19	0.8	613	9	CE171429	CE171429	tigr-gss-
	795	19	0.8	613	9	CE202458	CE202458	tigr-gss-
c	796	19	0.8	613	9	CE272758	CE272758	tigr-gss-
c	797	19	0.8	614	2	AW084703	AW084703	xa46ell.x
	798	19	0.8	614	5	BM944851	BM944851	UI-M-EH0p
	799	19	0.8	614	6	CA095251	CA095251	SCCCCL500
c	800	19	0.8	614	6	CD765300	CD765300	GGEZLB102
	801	19	0.8	614	8	BH031454	BH031454	RPCI-24-2
	802	19	0.8	614	9	CE068643	CE068643	tigr-gss-
c	803	19	0.8	614	9	CE206031	CE206031	tigr-gss-
c	804	19	0.8	614	9	CE353275	CE353275	tigr-gss-
c	805	19	0.8	615	9	CE042760	CE042760	tigr-gss-
	806	19	0.8	615	9	CE412403	CE412403	tigr-gss-

c 807	19	0.8	615	9	CE414297	CE414297	tigr-gss-
808	19	0.8	615	9	CE779412	CE779412	tigr-gss-
c 809	19	0.8	616	9	CE728853	CE728853	tigr-gss-
810	19	0.8	617	9	CE279831	CE279831	tigr-gss-
811	19	0.8	617	9	CE496887	CE496887	tigr-gss-
c 812	19	0.8	618	7	CN399820	CN399820	170004179
c 813	19	0.8	618	9	CE290403	CE290403	tigr-gss-
c 814	19	0.8	618	9	CE624805	CE624805	tigr-gss-
815	19	0.8	619	9	CE351280	CE351280	tigr-gss-
816	19	0.8	619	9	CE356630	CE356630	tigr-gss-
817	19	0.8	620	4	BM713814	BM713814	UI-E-EJ0-
c 818	19	0.8	620	9	CE837088	CE837088	tigr-gss-
c 819	19	0.8	621	5	BU704012	BU704012	UI-M-FO0-
820	19	0.8	621	7	CK332159	CK332159	H8192B02-
821	19	0.8	621	9	CE391609	CE391609	tigr-gss-
822	19	0.8	621	9	CE480466	CE480466	tigr-gss-
823	19	0.8	622	5	BU198134	BU198134	DCBCPD09
824	19	0.8	622	5	BU218077	BU218077	602883385
c 825	19	0.8	622	9	CE128017	CE128017	tigr-gss-
c 826	19	0.8	622	9	CE242081	CE242081	tigr-gss-
c 827	19	0.8	623	4	BG900730	BG900730	HOA6-1-E4
828	19	0.8	624	9	CE745905	CE745905	tigr-gss-
829	19	0.8	625	9	CE808290	CE808290	tigr-gss-
c 830	19	0.8	625	9	CE824882	CE824882	tigr-gss-
831	19	0.8	625	9	CG809240	CG809240	FSAAD79TR
c 832	19	0.8	626	9	CE115452	CE115452	tigr-gss-
c 833	19	0.8	626	9	CE340943	CE340943	tigr-gss-
834	19	0.8	626	9	CE356935	CE356935	tigr-gss-
835	19	0.8	628	9	CE429138	CE429138	tigr-gss-
c 836	19	0.8	628	9	CE697964	CE697964	tigr-gss-
c 837	19	0.8	628	9	CE796933	CE796933	tigr-gss-
838	19	0.8	629	9	CE852615	CE852615	tigr-gss-
839	19	0.8	630	9	CE181275	CE181275	tigr-gss-
840	19	0.8	630	9	CE654386	CE654386	tigr-gss-
c 841	19	0.8	630	9	CE749238	CE749238	tigr-gss-
842	19	0.8	631	7	CF361215	CF361215	827535 MA
c 843	19	0.8	631	9	CE402062	CE402062	tigr-gss-
844	19	0.8	631	9	CE750646	CE750646	tigr-gss-
845	19	0.8	631	9	CE843098	CE843098	tigr-gss-
c 846	19	0.8	632	9	CE244775	CE244775	tigr-gss-
c 847	19	0.8	632	9	CE363467	CE363467	tigr-gss-
c 848	19	0.8	632	9	CE436888	CE436888	tigr-gss-
849	19	0.8	633	6	CB816957	CB816957	dlgl9pz.r
c 850	19	0.8	633	8	AQ535941	AQ535941	RPCI-11-3
c 851	19	0.8	633	9	DR10I23S	AL749388	Danio rer
c 852	19	0.8	633	9	CE011262	CE011262	tigr-gss-
853	19	0.8	633	9	CE155736	CE155736	tigr-gss-
854	19	0.8	633	9	CE322554	CE322554	tigr-gss-
c 855	19	0.8	633	9	CE762808	CE762808	tigr-gss-
c 856	19	0.8	634	9	CE734545	CE734545	tigr-gss-
c 857	19	0.8	635	8	AZ829791	AZ829791	2M0107G12
858	19	0.8	635	9	CE219653	CE219653	tigr-gss-
c 859	19	0.8	635	9	CE303021	CE303021	tigr-gss-
860	19	0.8	636	9	CE079408	CE079408	tigr-gss-
c 861	19	0.8	638	9	CE378056	CE378056	tigr-gss-
862	19	0.8	638	9	CE491764	CE491764	tigr-gss-
c 863	19	0.8	638	9	CE811142	CE811142	tigr-gss-

c 864	19	0.8	639	6	CB456756	CB456756	714048	MA
c 865	19	0.8	639	9	CE269872	CE269872	tigr-gss-	
866	19	0.8	639	9	CE270215	CE270215	tigr-gss-	
c 867	19	0.8	639	9	CE681402	CE681402	tigr-gss-	
868	19	0.8	641	9	CE016761	CE016761	tigr-gss-	
c 869	19	0.8	642	5	BX329667	BX329667	BX329667	
c 870	19	0.8	642	9	CE071794	CE071794	tigr-gss-	
c 871	19	0.8	642	9	CE363790	CE363790	tigr-gss-	
c 872	19	0.8	642	9	CE473429	CE473429	tigr-gss-	
c 873	19	0.8	642	9	CE535428	CE535428	tigr-gss-	
874	19	0.8	642	9	CE675492	CE675492	tigr-gss-	
875	19	0.8	642	9	CE751509	CE751509	tigr-gss-	
876	19	0.8	642	9	CE759354	CE759354	tigr-gss-	
877	19	0.8	642	9	CE780349	CE780349	tigr-gss-	
c 878	19	0.8	643	6	CD094521	CD094521	ME1-0002G	
879	19	0.8	643	9	CE040210	CE040210	tigr-gss-	
880	19	0.8	643	9	CE515764	CE515764	tigr-gss-	
881	19	0.8	643	9	CE579639	CE579639	tigr-gss-	
c 882	19	0.8	643	9	CE678521	CE678521	tigr-gss-	
c 883	19	0.8	643	9	CE834604	CE834604	tigr-gss-	
884	19	0.8	644	5	BU364037	BU364037	603787470	
c 885	19	0.8	644	9	CE751874	CE751874	tigr-gss-	
c 886	19	0.8	645	9	CE191694	CE191694	tigr-gss-	
c 887	19	0.8	645	9	CE268503	CE268503	tigr-gss-	
c 888	19	0.8	645	9	CE427534	CE427534	tigr-gss-	
889	19	0.8	646	4	BM167840	BM167840	EST570363	
890	19	0.8	646	9	CE167458	CE167458	tigr-gss-	
891	19	0.8	646	9	CE554899	CE554899	tigr-gss-	
c 892	19	0.8	646	9	CE622412	CE622412	tigr-gss-	
c 893	19	0.8	647	9	CE254453	CE254453	tigr-gss-	
894	19	0.8	647	9	CE338170	CE338170	tigr-gss-	
c 895	19	0.8	647	9	CE643803	CE643803	tigr-gss-	
c 896	19	0.8	648	9	CE090826	CE090826	tigr-gss-	
897	19	0.8	648	9	CE512282	CE512282	tigr-gss-	
c 898	19	0.8	648	9	CE692179	CE692179	tigr-gss-	
899	19	0.8	648	9	CE735931	CE735931	tigr-gss-	
c 900	19	0.8	649	9	CE321965	CE321965	tigr-gss-	
901	19	0.8	649	9	CE398244	CE398244	tigr-gss-	
c 902	19	0.8	649	9	CE804754	CE804754	tigr-gss-	
c 903	19	0.8	650	9	CE068478	CE068478	tigr-gss-	
c 904	19	0.8	650	9	CE206106	CE206106	tigr-gss-	
905	19	0.8	650	9	CE305824	CE305824	tigr-gss-	
c 906	19	0.8	650	9	CE504643	CE504643	tigr-gss-	
c 907	19	0.8	651	8	BZ251692	BZ251692	CH230-306	
c 908	19	0.8	651	9	CE534710	CE534710	tigr-gss-	
909	19	0.8	651	9	CE722648	CE722648	tigr-gss-	
910	19	0.8	652	9	CE201197	CE201197	tigr-gss-	
c 911	19	0.8	652	9	CE253757	CE253757	tigr-gss-	
912	19	0.8	652	9	CE412769	CE412769	tigr-gss-	
c 913	19	0.8	652	9	CE679728	CE679728	tigr-gss-	
914	19	0.8	652	9	CE742518	CE742518	tigr-gss-	
c 915	19	0.8	652	9	CE802303	CE802303	tigr-gss-	
916	19	0.8	653	9	CE364543	CE364543	tigr-gss-	
c 917	19	0.8	653	9	CE669274	CE669274	tigr-gss-	
c 918	19	0.8	654	9	CL348273	CL348273	RPCI44_27	
919	19	0.8	656	9	CE225195	CE225195	tigr-gss-	
c 920	19	0.8	656	9	CE317406	CE317406	tigr-gss-	

	921	19	0.8	657	6	CA160888	CA160888	SCMCRZ306
	922	19	0.8	657	9	CE227726	CE227726	tigr-gss-
	923	19	0.8	658	9	CE262800	CE262800	tigr-gss-
c	924	19	0.8	658	9	CE301824	CE301824	tigr-gss-
	925	19	0.8	658	9	CE312659	CE312659	tigr-gss-
c	926	19	0.8	658	9	CE408208	CE408208	tigr-gss-
c	927	19	0.8	658	9	CE775750	CE775750	tigr-gss-
	928	19	0.8	659	9	CE122998	CE122998	tigr-gss-
	929	19	0.8	659	9	CE327319	CE327319	tigr-gss-
c	930	19	0.8	659	9	CE467179	CE467179	tigr-gss-
c	931	19	0.8	659	9	CE492930	CE492930	tigr-gss-
	932	19	0.8	659	9	CE502144	CE502144	tigr-gss-
	933	19	0.8	659	9	CE595018	CE595018	tigr-gss-
	934	19	0.8	660	5	BX404563	BX404563	BX404563
c	935	19	0.8	660	6	BY726304	BY726304	BY726304
	936	19	0.8	660	9	CE336605	CE336605	tigr-gss-
	937	19	0.8	660	9	CE345583	CE345583	tigr-gss-
c	938	19	0.8	660	9	CE400122	CE400122	tigr-gss-
	939	19	0.8	660	9	CE818444	CE818444	tigr-gss-
c	940	19	0.8	660	9	CE823742	CE823742	tigr-gss-
c	941	19	0.8	661	5	BU298539	BU298539	603740493
	942	19	0.8	661	8	BZ306400	BZ306400	hx42b11.b
	943	19	0.8	661	9	CE110665	CE110665	tigr-gss-
	944	19	0.8	661	9	CE383364	CE383364	tigr-gss-
	945	19	0.8	662	9	CE025178	CE025178	tigr-gss-
	946	19	0.8	662	9	CE519195	CE519195	tigr-gss-
c	947	19	0.8	663	8	BH503885	BH503885	BOHQJ43TR
	948	19	0.8	663	9	CE408699	CE408699	tigr-gss-
c	949	19	0.8	663	9	CE412381	CE412381	tigr-gss-
c	950	19	0.8	663	9	CE472613	CE472613	tigr-gss-
	951	19	0.8	664	6	CA196760	CA196760	SCBFAD109
	952	19	0.8	664	9	CE142136	CE142136	tigr-gss-
c	953	19	0.8	664	9	CE614068	CE614068	tigr-gss-
	954	19	0.8	665	9	AG088250	AG088250	Pan trogl
c	955	19	0.8	665	9	CE203400	CE203400	tigr-gss-
c	956	19	0.8	665	9	CE574445	CE574445	tigr-gss-
c	957	19	0.8	665	9	CE619544	CE619544	tigr-gss-
	958	19	0.8	665	9	CE809413	CE809413	tigr-gss-
c	959	19	0.8	665	9	CE839530	CE839530	tigr-gss-
c	960	19	0.8	666	2	BE855330	BE855330	ux5ld10.y
c	961	19	0.8	666	4	BI091323	BI091323	602855975
c	962	19	0.8	666	9	CE216908	CE216908	tigr-gss-
c	963	19	0.8	666	9	CE400580	CE400580	tigr-gss-
c	964	19	0.8	666	9	CE460531	CE460531	tigr-gss-
	965	19	0.8	666	9	CE643877	CE643877	tigr-gss-
	966	19	0.8	667	9	CE010806	CE010806	tigr-gss-
c	967	19	0.8	667	9	CE175489	CE175489	tigr-gss-
	968	19	0.8	667	9	CE195965	CE195965	tigr-gss-
	969	19	0.8	667	9	CE339784	CE339784	tigr-gss-
	970	19	0.8	667	9	CE630767	CE630767	tigr-gss-
	971	19	0.8	668	9	CE297162	CE297162	tigr-gss-
c	972	19	0.8	668	9	CE718910	CE718910	tigr-gss-
c	973	19	0.8	668	9	CE773634	CE773634	tigr-gss-
c	974	19	0.8	669	9	CE216980	CE216980	tigr-gss-
	975	19	0.8	669	9	CE315422	CE315422	tigr-gss-
c	976	19	0.8	669	9	CE750235	CE750235	tigr-gss-
c	977	19	0.8	669	9	CE825783	CE825783	tigr-gss-

c 978	19	0.8	670	9	CE618606	CE618606	tigr-gss-
c 979	19	0.8	671	7	CF785111	CF785111	AGENCOURT
c 980	19	0.8	671	9	CE271149	CE271149	tigr-gss-
c 981	19	0.8	671	9	CE272053	CE272053	tigr-gss-
982	19	0.8	671	9	CE343728	CE343728	tigr-gss-
983	19	0.8	671	9	CE831211	CE831211	tigr-gss-
984	19	0.8	672	8	BZ888251	BZ888251	CH240_257
c 985	19	0.8	672	9	CE018311	CE018311	tigr-gss-
c 986	19	0.8	672	9	CE784985	CE784985	tigr-gss-
987	19	0.8	672	9	CE787256	CE787256	tigr-gss-
988	19	0.8	673	6	CA812819	CA812819	CA48LN07I
989	19	0.8	673	9	BX971452	BX971452	Reverse s
990	19	0.8	673	9	CE112904	CE112904	tigr-gss-
c 991	19	0.8	673	9	CE124149	CE124149	tigr-gss-
992	19	0.8	673	9	CE428929	CE428929	tigr-gss-
993	19	0.8	674	9	CE595808	CE595808	tigr-gss-
c 994	19	0.8	674	9	CE809245	CE809245	tigr-gss-
c 995	19	0.8	674	9	CE847253	CE847253	tigr-gss-
996	19	0.8	675	9	AG043938	AG043938	Pan trogl
c 997	19	0.8	675	9	AG172133	AG172133	Pan trogl
c 998	19	0.8	676	7	CF113151	CF113151	Shultzomi
c 999	19	0.8	676	7	CN413937	CN413937	170005328
c1000	19	0.8	676	9	AG119646	AG119646	Pan trogl
1001	19	0.8	676	9	CE055616	CE055616	tigr-gss-
c1002	19	0.8	676	9	CE087647	CE087647	tigr-gss-
1003	19	0.8	676	9	CE409441	CE409441	tigr-gss-
c1004	19	0.8	676	9	CE443438	CE443438	tigr-gss-
1005	19	0.8	677	8	BH998337	BH998337	oei85f05.
1006	19	0.8	677	9	CE193106	CE193106	tigr-gss-
1007	19	0.8	677	9	CE284108	CE284108	tigr-gss-
1008	19	0.8	677	9	CE473122	CE473122	tigr-gss-
c1009	19	0.8	677	9	CE696564	CE696564	tigr-gss-
1010	19	0.8	678	5	BU235195	BU235195	603792853
c1011	19	0.8	678	9	CE283255	CE283255	tigr-gss-
c1012	19	0.8	678	9	CE622999	CE622999	tigr-gss-
1013	19	0.8	678	9	CE694742	CE694742	tigr-gss-
c1014	19	0.8	679	9	CE544794	CE544794	tigr-gss-
c1015	19	0.8	680	6	CB169100	CB169100	IMU602702
1016	19	0.8	680	8	BZ087618	BZ087618	lkg67h10.
1017	19	0.8	680	9	CE093549	CE093549	tigr-gss-
1018	19	0.8	680	9	CE288191	CE288191	tigr-gss-
c1019	19	0.8	680	9	CE724945	CE724945	tigr-gss-
1020	19	0.8	680	9	CE771859	CE771859	tigr-gss-
c1021	19	0.8	681	7	CK748526	CK748526	pam01-lms
1022	19	0.8	681	9	CE103692	CE103692	tigr-gss-
c1023	19	0.8	681	9	CE192506	CE192506	tigr-gss-
c1024	19	0.8	681	9	CE195317	CE195317	tigr-gss-
1025	19	0.8	681	9	CE517696	CE517696	tigr-gss-
c1026	19	0.8	681	9	CE560119	CE560119	tigr-gss-
c1027	19	0.8	681	9	CE676880	CE676880	tigr-gss-
c1028	19	0.8	682	6	CA374470	CA374470	648902 NC
1029	19	0.8	682	9	CE565033	CE565033	tigr-gss-
c1030	19	0.8	683	7	CF235569	CF235569	PtaJXT002
c1031	19	0.8	683	9	AG211589	AG211589	Oryza sat
c1032	19	0.8	683	9	CE251727	CE251727	tigr-gss-
1033	19	0.8	683	9	CE489518	CE489518	tigr-gss-
c1034	19	0.8	683	9	CE494365	CE494365	tigr-gss-

c1035	19	0.8	684	6	BY720132	BY720132	BY720132
1036	19	0.8	684	9	CE057124	CE057124	tigr-gss-
1037	19	0.8	684	9	CE207772	CE207772	tigr-gss-
c1038	19	0.8	684	9	CE345446	CE345446	tigr-gss-
c1039	19	0.8	685	9	CR127048	CR127048	Reverse s
1040	19	0.8	685	9	CE607430	CE607430	tigr-gss-
c1041	19	0.8	685	9	CE847625	CE847625	tigr-gss-
1042	19	0.8	686	6	CA291576	CA291576	SCCCNR100
1043	19	0.8	686	6	CD728541	CD728541	4034413 1
1044	19	0.8	686	8	BH942339	BH942339	odg48d04.
1045	19	0.8	686	9	CE069483	CE069483	tigr-gss-
1046	19	0.8	686	9	CE296171	CE296171	tigr-gss-
1047	19	0.8	686	9	CE542430	CE542430	tigr-gss-
1048	19	0.8	686	9	CE791904	CE791904	tigr-gss-
c1049	19	0.8	687	7	CN399821	CN399821	170004251
1050	19	0.8	687	8	B76321	B76321	RPCI11-1401
1051	19	0.8	687	8	BH996696	BH996696	oef89c08.
c1052	19	0.8	688	9	CE096962	CE096962	tigr-gss-
1053	19	0.8	688	9	CE357514	CE357514	tigr-gss-
1054	19	0.8	689	8	BZ935402	BZ935402	CH240_85A
1055	19	0.8	689	9	CE190232	CE190232	tigr-gss-
c1056	19	0.8	689	9	CE209595	CE209595	tigr-gss-
1057	19	0.8	689	9	CE438037	CE438037	tigr-gss-
1058	19	0.8	689	9	CE763734	CE763734	tigr-gss-
1059	19	0.8	690	7	CR754500	CR754500	CR754500
c1060	19	0.8	690	7	CR755770	CR755770	CR755770
c1061	19	0.8	690	8	AZ979594	AZ979594	2M0256P14
1062	19	0.8	690	8	BH932541	BH932541	odh46h01.
c1063	19	0.8	690	9	CE072967	CE072967	tigr-gss-
1064	19	0.8	690	9	CE076568	CE076568	tigr-gss-
c1065	19	0.8	690	9	CE103838	CE103838	tigr-gss-
c1066	19	0.8	690	9	CE118541	CE118541	tigr-gss-
c1067	19	0.8	690	9	CE155228	CE155228	tigr-gss-
c1068	19	0.8	690	9	CE162930	CE162930	tigr-gss-
c1069	19	0.8	690	9	CE187076	CE187076	tigr-gss-
1070	19	0.8	690	9	CE421217	CE421217	tigr-gss-
c1071	19	0.8	690	9	CE583386	CE583386	tigr-gss-
c1072	19	0.8	690	9	CE622192	CE622192	tigr-gss-
1073	19	0.8	691	9	CE058472	CE058472	tigr-gss-
1074	19	0.8	691	9	CE125003	CE125003	tigr-gss-
c1075	19	0.8	691	9	CE371066	CE371066	tigr-gss-
1076	19	0.8	691	9	CE843985	CE843985	tigr-gss-
c1077	19	0.8	692	5	BU005981	BU005981	QGG9J22.y
c1078	19	0.8	692	8	BH998217	BH998217	oed82d11.
c1079	19	0.8	692	9	CE077826	CE077826	tigr-gss-
1080	19	0.8	692	9	CE190755	CE190755	tigr-gss-
c1081	19	0.8	692	9	CE339383	CE339383	tigr-gss-
c1082	19	0.8	693	9	CE328968	CE328968	tigr-gss-
1083	19	0.8	693	9	CE643726	CE643726	tigr-gss-
1084	19	0.8	693	9	CE770048	CE770048	tigr-gss-
1085	19	0.8	693	9	CE842871	CE842871	tigr-gss-
1086	19	0.8	694	9	CE460176	CE460176	tigr-gss-
c1087	19	0.8	694	9	CE726688	CE726688	tigr-gss-
c1088	19	0.8	695	9	CE222639	CE222639	tigr-gss-
c1089	19	0.8	695	9	CE355064	CE355064	tigr-gss-
c1090	19	0.8	695	9	CE764235	CE764235	tigr-gss-
c1091	19	0.8	696	9	CE059559	CE059559	tigr-gss-

1092	19	0.8	696	9	CE442615	CE442615	tigr-gss-
1093	19	0.8	696	9	CE649986	CE649986	tigr-gss-
c1094	19	0.8	696	9	CE706630	CE706630	tigr-gss-
1095	19	0.8	697	9	CNS0485I	AL278847	Tetraodon
c1096	19	0.8	697	9	CE601022	CE601022	tigr-gss-
1097	19	0.8	697	9	CE836969	CE836969	tigr-gss-
1098	19	0.8	698	8	BH979207	BH979207	ode94c03.
c1099	19	0.8	698	9	CE181348	CE181348	tigr-gss-
c1100	19	0.8	699	9	CE143497	CE143497	tigr-gss-
1101	19	0.8	699	9	CE665692	CE665692	tigr-gss-
c1102	19	0.8	699	9	CE818161	CE818161	tigr-gss-
1103	19	0.8	700	8	BZ419915	BZ419915	if61h03.b
c1104	19	0.8	700	9	CE071758	CE071758	tigr-gss-
c1105	19	0.8	700	9	CE163684	CE163684	tigr-gss-
1106	19	0.8	701	8	BH928951	BH928951	odh29f05.
c1107	19	0.8	701	8	BH940396	BH940396	odf76b09.
1108	19	0.8	701	9	CE786141	CE786141	tigr-gss-
1109	19	0.8	702	6	CD906384	CD906384	G468.104L
c1110	19	0.8	702	9	CE073757	CE073757	tigr-gss-
1111	19	0.8	702	9	CE177133	CE177133	tigr-gss-
c1112	19	0.8	702	9	CE543289	CE543289	tigr-gss-
c1113	19	0.8	703	9	CE442264	CE442264	tigr-gss-
1114	19	0.8	703	9	CE505523	CE505523	tigr-gss-
c1115	19	0.8	703	9	CE561655	CE561655	tigr-gss-
1116	19	0.8	704	8	AZ993875	AZ993875	2M0279P06
c1117	19	0.8	704	9	CE100432	CE100432	tigr-gss-
1118	19	0.8	704	9	CE537407	CE537407	tigr-gss-
c1119	19	0.8	704	9	CE552328	CE552328	tigr-gss-
c1120	19	0.8	704	9	CE651429	CE651429	tigr-gss-
c1121	19	0.8	705	5	BU224882	BU224882	603801186
1122	19	0.8	705	9	CE039952	CE039952	tigr-gss-
c1123	19	0.8	705	9	CE207786	CE207786	tigr-gss-
c1124	19	0.8	705	9	CE422051	CE422051	tigr-gss-
1125	19	0.8	705	9	CE445743	CE445743	tigr-gss-
c1126	19	0.8	705	9	CE553023	CE553023	tigr-gss-
c1127	19	0.8	705	9	CE582192	CE582192	tigr-gss-
c1128	19	0.8	706	9	CE035700	CE035700	tigr-gss-
1129	19	0.8	706	9	CE278911	CE278911	tigr-gss-
c1130	19	0.8	706	9	CE469153	CE469153	tigr-gss-
c1131	19	0.8	706	9	CE696467	CE696467	tigr-gss-
1132	19	0.8	708	4	BJ791749	BJ791749	BJ791749
c1133	19	0.8	708	6	BY729901	BY729901	BY729901
c1134	19	0.8	708	9	CE205928	CE205928	tigr-gss-
c1135	19	0.8	709	5	BM978029	BM978029	UI-CF-EC1
c1136	19	0.8	709	9	CE003499	CE003499	tigr-gss-
1137	19	0.8	709	9	CE372392	CE372392	tigr-gss-
c1138	19	0.8	709	9	CE415609	CE415609	tigr-gss-
1139	19	0.8	709	9	CE462458	CE462458	tigr-gss-
1140	19	0.8	710	4	BJ782535	BJ782535	BJ782535
1141	19	0.8	710	8	BZ072320	BZ072320	lke36e07.
1142	19	0.8	710	9	CE318529	CE318529	tigr-gss-
c1143	19	0.8	710	9	CE637142	CE637142	tigr-gss-
c1144	19	0.8	711	9	CE035077	CE035077	tigr-gss-
1145	19	0.8	711	9	CE313950	CE313950	tigr-gss-
1146	19	0.8	712	8	BH932000	BH932000	odj16d03.
1147	19	0.8	712	9	CE135206	CE135206	tigr-gss-
c1148	19	0.8	712	9	CE165873	CE165873	tigr-gss-

c1149	19	0.8	712	9	CE302854	CE302854	tigr-gss-
1150	19	0.8	712	9	CE811643	CE811643	tigr-gss-
c1151	19	0.8	712	9	CE827426	CE827426	tigr-gss-
1152	19	0.8	713	6	BY732332	BY732332	BY732332
c1153	19	0.8	713	8	BZ027265	BZ027265	oehl7f05.
1154	19	0.8	713	9	CE053592	CE053592	tigr-gss-
c1155	19	0.8	713	9	CE214862	CE214862	tigr-gss-
c1156	19	0.8	713	9	CE217260	CE217260	tigr-gss-
1157	19	0.8	713	9	CE366448	CE366448	tigr-gss-
1158	19	0.8	713	9	CE393829	CE393829	tigr-gss-
1159	19	0.8	713	9	CE457088	CE457088	tigr-gss-
1160	19	0.8	713	9	CE668075	CE668075	tigr-gss-
c1161	19	0.8	714	7	CN296741	CN296741	170004706
c1162	19	0.8	714	9	CE272707	CE272707	tigr-gss-
c1163	19	0.8	714	9	CE717136	CE717136	tigr-gss-
1164	19	0.8	714	9	CE749086	CE749086	tigr-gss-
1165	19	0.8	714	9	CE804604	CE804604	tigr-gss-
1166	19	0.8	714	9	CE808542	CE808542	tigr-gss-
c1167	19	0.8	714	9	CE851635	CE851635	tigr-gss-
c1168	19	0.8	715	9	AG406459	AG406459	Mus muscu
c1169	19	0.8	715	9	CE494450	CE494450	tigr-gss-
c1170	19	0.8	715	9	CE767498	CE767498	tigr-gss-
c1171	19	0.8	716	5	BU247361	BU247361	603592373
c1172	19	0.8	716	7	CR285236	CR285236	CR285236
c1173	19	0.8	716	9	CC498059	CC498059	CH240_335
c1174	19	0.8	716	9	CE302113	CE302113	tigr-gss-
1175	19	0.8	716	9	CE573156	CE573156	tigr-gss-
1176	19	0.8	717	8	BH597760	BH597760	BOGMV30TR
c1177	19	0.8	717	9	CE077191	CE077191	tigr-gss-
c1178	19	0.8	718	9	CE364041	CE364041	tigr-gss-
c1179	19	0.8	719	9	AG415998	AG415998	Mus muscu
1180	19	0.8	719	9	CE287399	CE287399	tigr-gss-
c1181	19	0.8	719	9	CE347083	CE347083	tigr-gss-
c1182	19	0.8	720	9	CE078107	CE078107	tigr-gss-
c1183	19	0.8	720	9	CE153698	CE153698	tigr-gss-
c1184	19	0.8	720	9	CE190397	CE190397	tigr-gss-
c1185	19	0.8	720	9	CE486019	CE486019	tigr-gss-
c1186	19	0.8	720	9	CE576256	CE576256	tigr-gss-
1187	19	0.8	721	9	CE139984	CE139984	tigr-gss-
c1188	19	0.8	721	9	CE157771	CE157771	tigr-gss-
c1189	19	0.8	721	9	CE649902	CE649902	tigr-gss-
1190	19	0.8	722	9	CC567481	CC567481	CH240_441
c1191	19	0.8	722	9	CE276893	CE276893	tigr-gss-
c1192	19	0.8	722	9	CE385019	CE385019	tigr-gss-
c1193	19	0.8	723	8	BH670086	BH670086	BOHSR07TF
c1194	19	0.8	723	9	CE015839	CE015839	tigr-gss-
1195	19	0.8	723	9	CE118039	CE118039	tigr-gss-
c1196	19	0.8	723	9	CE418337	CE418337	tigr-gss-
c1197	19	0.8	723	9	CE771675	CE771675	tigr-gss-
c1198	19	0.8	724	9	CE438264	CE438264	tigr-gss-
c1199	19	0.8	725	9	CE087038	CE087038	tigr-gss-
c1200	19	0.8	725	9	CE104319	CE104319	tigr-gss-
c1201	19	0.8	725	9	CE474110	CE474110	tigr-gss-
c1202	19	0.8	725	9	CE624683	CE624683	tigr-gss-
c1203	19	0.8	725	9	CE742506	CE742506	tigr-gss-
c1204	19	0.8	726	5	BX956930	BX956930	DKFZp781C
1205	19	0.8	726	8	BH461010	BH461010	BOGBO64TR

c1206	19	0.8	727	9	CE389906	CE389906	tigr-gss-
c1207	19	0.8	727	9	CE715279	CE715279	tigr-gss-
c1208	19	0.8	727	9	CE734942	CE734942	tigr-gss-
c1209	19	0.8	727	9	CE749709	CE749709	tigr-gss-
c1210	19	0.8	727	9	CE776259	CE776259	tigr-gss-
c1211	19	0.8	728	8	BZ434030	BZ434030	BONAF08TR
c1212	19	0.8	728	8	BZ497694	BZ497694	BONMW83TF
c1213	19	0.8	728	9	CE081289	CE081289	tigr-gss-
c1214	19	0.8	728	9	CE210294	CE210294	tigr-gss-
c1215	19	0.8	728	9	CE326692	CE326692	tigr-gss-
c1216	19	0.8	728	9	CE756238	CE756238	tigr-gss-
c1217	19	0.8	728	9	CE769128	CE769128	tigr-gss-
1218	19	0.8	729	8	BH703303	BH703303	BOHUY82TR
c1219	19	0.8	729	9	CE140951	CE140951	tigr-gss-
c1220	19	0.8	729	9	CE231955	CE231955	tigr-gss-
1221	19	0.8	729	9	CE351162	CE351162	tigr-gss-
1222	19	0.8	729	9	CE443696	CE443696	tigr-gss-
c1223	19	0.8	729	9	CE676503	CE676503	tigr-gss-
c1224	19	0.8	730	6	CD906841	CD906841	G468.105J
1225	19	0.8	730	9	AG403799	AG403799	Mus muscu
c1226	19	0.8	730	9	CE059978	CE059978	tigr-gss-
1227	19	0.8	730	9	CE618099	CE618099	tigr-gss-
c1228	19	0.8	731	5	BU285139	BU285139	603864696
c1229	19	0.8	731	9	AG433363	AG433363	Mus muscu
1230	19	0.8	731	9	CR800768	CR800768	GR0AAA2CA
c1231	19	0.8	731	9	CE017092	CE017092	tigr-gss-
c1232	19	0.8	731	9	CE608851	CE608851	tigr-gss-
c1233	19	0.8	731	9	CE802753	CE802753	tigr-gss-
c1234	19	0.8	732	9	CE098234	CE098234	tigr-gss-
1235	19	0.8	732	9	CE187621	CE187621	tigr-gss-
c1236	19	0.8	732	9	CE843130	CE843130	tigr-gss-
1237	19	0.8	733	8	BH992753	BH992753	oed84d01.
1238	19	0.8	733	8	BZ485635	BZ485635	BONRP37TR
c1239	19	0.8	733	9	CE049548	CE049548	tigr-gss-
c1240	19	0.8	734	4	BG719818	BG719818	602691226
c1241	19	0.8	734	9	CE591681	CE591681	tigr-gss-
c1242	19	0.8	735	9	CE684232	CE684232	tigr-gss-
c1243	19	0.8	735	9	CG342154	CG342154	OGVGC47TH
c1244	19	0.8	736	9	CE786200	CE786200	tigr-gss-
1245	19	0.8	737	7	CO567098	CO567098	AGENCOURT
c1246	19	0.8	737	9	CE659849	CE659849	tigr-gss-
1247	19	0.8	738	9	CE327604	CE327604	tigr-gss-
c1248	19	0.8	739	9	CE192890	CE192890	tigr-gss-
c1249	19	0.8	739	9	CE340404	CE340404	tigr-gss-
c1250	19	0.8	739	9	CE458130	CE458130	tigr-gss-
c1251	19	0.8	739	9	CE779095	CE779095	tigr-gss-
c1252	19	0.8	740	9	CE302237	CE302237	tigr-gss-
c1253	19	0.8	741	8	BH606419	BH606419	BOGFM10TR
c1254	19	0.8	741	8	BH937592	BH937592	odg57e02.
1255	19	0.8	741	8	AQ582716	AQ582716	RPCI-11-4
c1256	19	0.8	741	9	CE351502	CE351502	tigr-gss-
c1257	19	0.8	741	9	CE493127	CE493127	tigr-gss-
c1258	19	0.8	741	9	CE623526	CE623526	tigr-gss-
c1259	19	0.8	742	9	CE590970	CE590970	tigr-gss-
c1260	19	0.8	743	9	CE157867	CE157867	tigr-gss-
c1261	19	0.8	743	9	CE291430	CE291430	tigr-gss-
1262	19	0.8	743	9	CE827492	CE827492	tigr-gss-

c1263	19	0.8	744	9	CE386062	CE386062	tigr-gss-
c1264	19	0.8	744	9	CE426947	CE426947	tigr-gss-
1265	19	0.8	744	9	CE573679	CE573679	tigr-gss-
c1266	19	0.8	745	9	CE122468	CE122468	tigr-gss-
c1267	19	0.8	745	9	CE747647	CE747647	tigr-gss-
c1268	19	0.8	746	9	AG454470	AG454470	Mus muscu
c1269	19	0.8	746	9	AG571147	AG571147	Mus muscu
c1270	19	0.8	746	9	CE429845	CE429845	tigr-gss-
c1271	19	0.8	746	9	CE468182	CE468182	tigr-gss-
1272	19	0.8	746	9	CE573824	CE573824	tigr-gss-
1273	19	0.8	747	9	CE121743	CE121743	tigr-gss-
c1274	19	0.8	747	9	CE123201	CE123201	tigr-gss-
1275	19	0.8	748	8	BZ396654	BZ396654	EINAQ56TR
c1276	19	0.8	748	9	AG492780	AG492780	Mus muscu
1277	19	0.8	748	9	CE218398	CE218398	tigr-gss-
c1278	19	0.8	748	9	CE457596	CE457596	tigr-gss-
1279	19	0.8	749	9	CE224436	CE224436	tigr-gss-
1280	19	0.8	750	8	BH122972	BH122972	RPCI-24-2
c1281	19	0.8	750	9	CE471066	CE471066	tigr-gss-
c1282	19	0.8	750	9	CE779100	CE779100	tigr-gss-
c1283	19	0.8	750	9	CE847179	CE847179	tigr-gss-
c1284	19	0.8	751	9	CE799085	CE799085	tigr-gss-
c1285	19	0.8	752	7	CK474028	CK474028	AGENCOURT
c1286	19	0.8	752	9	CE052741	CE052741	tigr-gss-
c1287	19	0.8	752	9	CE108352	CE108352	tigr-gss-
1288	19	0.8	752	9	CE132472	CE132472	tigr-gss-
c1289	19	0.8	752	9	CE323070	CE323070	tigr-gss-
c1290	19	0.8	753	9	CE330308	CE330308	tigr-gss-
c1291	19	0.8	754	5	BU260339	BU260339	603502283
1292	19	0.8	755	4	BJ795984	BJ795984	BJ795984
1293	19	0.8	755	9	CL750592	CL750592	OR_BBa011
c1294	19	0.8	756	9	AG589902	AG589902	Mus muscu
c1295	19	0.8	756	9	CE683828	CE683828	tigr-gss-
c1296	19	0.8	757	8	BZ502888	BZ502888	BONMK14TR
1297	19	0.8	758	4	BI819345	BI819345	603034505
c1298	19	0.8	758	8	BH924361	BH924361	odi55a04.
c1299	19	0.8	760	8	BH478501	BH478501	BOHAJ54TR
c1300	19	0.8	760	9	CE576742	CE576742	tigr-gss-
c1301	19	0.8	761	8	AZ623852	AZ623852	1M0462A03
1302	19	0.8	761	8	BZ060851	BZ060851	ljul0b03.
c1303	19	0.8	761	9	CE291455	CE291455	tigr-gss-
c1304	19	0.8	763	9	CR275365	CR275365	Reverse s
c1305	19	0.8	763	9	CE375441	CE375441	tigr-gss-
c1306	19	0.8	763	9	CE432049	CE432049	tigr-gss-
c1307	19	0.8	764	9	AG487347	AG487347	Mus muscu
c1308	19	0.8	764	9	CE062499	CE062499	tigr-gss-
c1309	19	0.8	764	9	CE331849	CE331849	tigr-gss-
c1310	19	0.8	766	9	CE280593	CE280593	tigr-gss-
c1311	19	0.8	766	9	CE569560	CE569560	tigr-gss-
1312	19	0.8	767	5	BU854442	BU854442	AGENCOURT
1313	19	0.8	767	9	CE086450	CE086450	tigr-gss-
c1314	19	0.8	767	9	CE717068	CE717068	tigr-gss-
1315	19	0.8	768	8	BZ180286	BZ180286	CH230-434
c1316	19	0.8	768	9	CE308947	CE308947	tigr-gss-
c1317	19	0.8	769	9	CE238714	CE238714	tigr-gss-
c1318	19	0.8	770	9	CE317307	CE317307	tigr-gss-
c1319	19	0.8	771	9	CE246607	CE246607	tigr-gss-

c1320	19	0.8	773	9	CE827643	CE827643	tigr-gss-
1321	19	0.8	774	4	BG753925	BG753925	602709446
1322	19	0.8	774	8	BH478920	BH478920	BOGWN41TR
c1323	19	0.8	775	9	AG523838	AG523838	Mus muscu
c1324	19	0.8	776	9	CL135735	CL135735	ISB1-106P
1325	19	0.8	777	9	CE730042	CE730042	tigr-gss-
c1326	19	0.8	779	9	CR823371	CR823371	GR0AAA53C
c1327	19	0.8	779	9	CE026588	CE026588	tigr-gss-
c1328	19	0.8	780	9	CR274821	CR274821	Forward s
c1329	19	0.8	781	5	BU465345	BU465345	603369485
1330	19	0.8	781	8	BZ392975	BZ392975	EINAM01TF
1331	19	0.8	781	8	BZ610446	BZ610446	WHACW68TR
c1332	19	0.8	782	9	CE404635	CE404635	tigr-gss-
1333	19	0.8	783	7	CO363325	CO363325	RTK1_9_B1
1334	19	0.8	783	8	BZ513134	BZ513134	BOMQL26TF
1335	19	0.8	785	8	BH726536	BH726536	BOMDR44TF
1336	19	0.8	786	9	CE820882	CE820882	tigr-gss-
c1337	19	0.8	788	9	CR257365	CR257365	Reverse s
1338	19	0.8	793	7	CF256209	CF256209	mdvn137_b
c1339	19	0.8	794	5	BU382423	BU382423	603861509
c1340	19	0.8	797	5	BP163963	BP163963	BP163963
1341	19	0.8	797	8	BZ410657	BZ410657	OGACC75TM
1342	19	0.8	798	2	BE544133	BE544133	601076669
1343	19	0.8	798	5	BQ687097	BQ687097	AGENCOURT
c1344	19	0.8	799	5	BU327530	BU327530	603406292
c1345	19	0.8	800	4	BG167946	BG167946	602340041
1346	19	0.8	802	4	BM162880	BM162880	EST565403
1347	19	0.8	802	4	BM164694	BM164694	EST567217
c1348	19	0.8	804	9	CG175327	CG175327	PUIEO44TD
1349	19	0.8	804	9	CG966119	CG966119	MBEIB41TF
c1350	19	0.8	805	9	CR230142	CR230142	Forward s
c1351	19	0.8	805	9	CL957676	CL957676	OsIRUA000
c1352	19	0.8	806	6	CA266956	CA266956	SCRFLB206
1353	19	0.8	806	7	CK196084	CK196084	FGAS00453
1354	19	0.8	807	6	CA812768	CA812768	CA48LN07I
1355	19	0.8	809	8	BH649410	BH649410	BOMAF05TF
1356	19	0.8	810	9	CR274398	CR274398	Reverse s
c1357	19	0.8	812	4	BI758489	BI758489	603023334
c1358	19	0.8	814	8	BH573522	BH573522	BOGYW17TF
1359	19	0.8	816	8	CC395073	CC395073	PUHAY16TD
c1360	19	0.8	817	4	BM360844	BM360844	GA_Ea003
c1361	19	0.8	817	8	BZ246890	BZ246890	CH230-325
c1362	19	0.8	817	9	CR114033	CR114033	Reverse s
1363	19	0.8	818	4	BI732082	BI732082	603352870
c1364	19	0.8	818	9	CR033021	CR033021	Reverse s
1365	19	0.8	819	7	CK238077	CK238077	AGENCOURT
1366	19	0.8	819	8	CC199510	CC199510	ZMMBBc032
1367	19	0.8	820	8	BZ471347	BZ471347	BONGV68TF
1368	19	0.8	820	9	CC805897	CC805897	ZMMBBc046
c1369	19	0.8	822	9	CL301194	CL301194	gbs08_CH2
c1370	19	0.8	823	5	BU362418	BU362418	603784642
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1372	19	0.8	827	7	CN823337	CN823337	Oa_splbn
c1373	19	0.8	830	9	CR094185	CR094185	Reverse s
c1374	19	0.8	832	5	BU420520	BU420520	603955117
c1375	19	0.8	833	8	BH463106	BH463106	BOGZV24TR
1376	19	0.8	836	7	CK197204	CK197204	FGAS00567

1377	19	0.8	836	7	CK395412	CK395412	AGENCOURT
c1378	19	0.8	837	8	BH535517	BH535517	BOHOK70TF
c1379	19	0.8	837	8	BH594142	BH594142	BOGWZ48TF
1380	19	0.8	838	8	BH709341	BH709341	BOHXS96TF
c1381	19	0.8	839	7	CO485027	CO485027	GQ0206.TB
1382	19	0.8	840	9	CC720879	CC720879	OGMAV35TH
1383	19	0.8	844	6	CD325893	CD325893	AGENCOURT
c1384	19	0.8	845	9	CR135205	CR135205	Reverse s
c1385	19	0.8	848	6	CD643411	CD643411	AGENCOURT
1386	19	0.8	853	8	BH705190	BH705190	BOHUS10TF
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c1388	19	0.8	853	8	CC395070	CC395070	PUHAY16TB
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1390	19	0.8	858	7	CV236957	CV236957	WS01226.B
1391	19	0.8	860	8	AZ046318	AZ046318	nbeb0091P
1392	19	0.8	860	8	BZ224049	BZ224049	CH230-260
c1393	19	0.8	862	9	BX988666	BX988666	Reverse s
1394	19	0.8	866	8	BH596501	BH596501	BOGZY74TF
c1395	19	0.8	866	8	BH720198	BH720198	BOHZV36TF
c1396	19	0.8	867	8	BZ640953	BZ640953	OGCAX06TC
1397	19	0.8	868	9	CNS01NIT	AL152278	Anopheles
c1398	19	0.8	869	6	CA279117	CA279117	SCBFRT309
c1399	19	0.8	870	9	CR065595	CR065595	Reverse s
c1400	19	0.8	871	9	CL311713	CL311713	290998_LB
1401	19	0.8	873	9	CR015977	CR015977	Reverse s
c1402	19	0.8	873	9	CR242647	CR242647	Forward s
1403	19	0.8	877	8	CC378867	CC378867	PUHTX49TD
c1404	19	0.8	879	7	CV435383	CV435383	58928.1 S
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c1406	19	0.8	884	4	BI663264	BI663264	603287307
1407	19	0.8	888	5	BU372222	BU372222	603812471
c1408	19	0.8	889	6	CA164571	CA164571	SCACRZ303
c1409	19	0.8	894	9	CR138136	CR138136	Forward s
1410	19	0.8	895	7	CO985868	CO985868	GM89015B1
c1411	19	0.8	902	9	CR047917	CR047917	Forward s
1412	19	0.8	907	5	BX342106	BX342106	BX342106
c1413	19	0.8	907	7	CK021524	CK021524	AGENCOURT
1414	19	0.8	907	8	CC433385	CC433385	PUHPK62TD
c1415	19	0.8	908	5	BU110316	BU110316	603127962
1416	19	0.8	909	2	BF100648	BF100648	601754181
c1417	19	0.8	912	9	CR269741	CR269741	Forward s
c1418	19	0.8	914	1	AV383794	AV383794	AV383794
c1419	19	0.8	915	7	CO019038	CO019038	EST815131
c1420	19	0.8	924	4	BI195155	BI195155	602944163
1421	19	0.8	924	9	CR041053	CR041053	Forward s
c1422	19	0.8	926	5	BX392121	BX392121	BX392121
c1423	19	0.8	927	2	BE421230	BE421230	HWM007.B0
c1424	19	0.8	927	8	BH136483	BH136483	ENTPC05TF
1425	19	0.8	928	9	CG064409	CG064409	PUII081TB
1426	19	0.8	930	8	CC381236	CC381236	PUHT049TD
1427	19	0.8	933	9	CG191208	CG191208	PUJFE62TD
c1428	19	0.8	934	9	CL135068	CL135068	ISB1-105P
1429	19	0.8	935	9	CG062770	CG062770	PUJCK73TD
c1430	19	0.8	936	1	AL528153	AL528153	AL528153
c1431	19	0.8	936	5	BQ233428	BQ233428	AGENCOURT
1432	19	0.8	936	9	CC720286	CC720286	OGOBJ34TV
c1433	19	0.8	937	4	BG431828	BG431828	602498245

c1434	19	0.8	942	7	CN024707	CN024707	AGENCOURT
1435	19	0.8	944	5	BQ644298	BQ644298	AGENCOURT
1436	19	0.8	945	5	BQ920325	BQ920325	AGENCOURT
c1437	19	0.8	950	4	BG176642	BG176642	602313233
c1438	19	0.8	951	9	CG950145	CG950145	MBELC53TR
1439	19	0.8	956	3	CNS08HGB	BX012039	Single re
c1440	19	0.8	961	3	CNS08HGA	BX012038	Single re
1441	19	0.8	962	4	BM564748	BM564748	AGENCOURT
c1442	19	0.8	964	7	CO021452	CO021452	EST817545
1443	19	0.8	976	6	CB558602	CB558602	AGENCOURT
c1444	19	0.8	981	9	CNS03XK2	AL265115	Tetraodon
c1445	19	0.8	995	2	BE874561	BE874561	601489675
1446	19	0.8	999	6	BY703340	BY703340	BY703340
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c1448	19	0.8	1027	5	BU839991	BU839991	AGENCOURT
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1451	19	0.8	1035	6	BY710380	BY710380	BY710380
1452	19	0.8	1041	8	CC208131	CC208131	CH261-101
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1455	19	0.8	1079	9	CNS05A0K	AL327917	Tetraodon
1456	19	0.8	1104	9	CL066126	CL066126	CH216-108
c1457	19	0.8	1105	8	BZ558839	BZ558839	pacs2-164
1458	19	0.8	1108	9	CL084072	CL084072	ISB1-2N8
1459	19	0.8	1115	8	CC240393	CC240393	CH261-187
1460	19	0.8	1118	8	BZ695338	BZ695338	SP_Ba006
c1461	19	0.8	1119	9	CL026139	CL026139	CH216-22K
c1462	19	0.8	1120	1	AL535310	AL535310	AL535310
1463	19	0.8	1137	3	AK011093	AK011093	Mus muscu
1464	19	0.8	1145	3	AK010997	AK010997	Mus muscu
1465	19	0.8	1148	8	BZ566016	BZ566016	pacs2-164
1466	19	0.8	1156	7	CN642903	CN642903	ILLUMIGEN
1467	19	0.8	1166	9	AG391351	AG391351	Mus muscu
1468	19	0.8	1196	8	CC228428	CC228428	CH261-157
c1469	19	0.8	1206	8	CC274268	CC274268	CH261-20E
c1470	19	0.8	1208	8	B10713	B10713	F20L14-T7 I
c1471	19	0.8	1229	5	BQ938033	BQ938033	AGENCOURT
1472	19	0.8	1239	5	BQ073691	BQ073691	AGENCOURT
c1473	19	0.8	1268	3	CR729855	CR729855	Tetraodon
1474	19	0.8	1275	9	CL953223	CL953223	OsJRUA000
c1475	19	0.8	1280	3	CR731214	CR731214	Tetraodon
c1476	19	0.8	1285	3	CR692694	CR692694	Tetraodon
c1477	19	0.8	1316	9	CG755342	CG755342	P051-1-B0
c1478	19	0.8	1329	3	CR661548	CR661548	Tetraodon
1479	19	0.8	1333	9	AG170919	AG170919	Pan trogl
c1480	19	0.8	1337	3	CR731636	CR731636	Tetraodon
1481	19	0.8	1523	2	BE548217	BE548217	601074276
c1482	19	0.8	1778	6	CD385837	CD385837	AGENCOURT
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c1484	19	0.8	2024	3	AK039504	AK039504	Mus muscu
1485	19	0.8	2086	9	AY420699	AY420699	Homo sapi
1486	19	0.8	2086	9	AY420701	AY420701	Mus muscu
c1487	19	0.8	2235	3	AK077792	AK077792	Mus muscu
1488	19	0.8	2355	3	AK002841	AK002841	Mus muscu
1489	19	0.8	2547	9	AY418202	AY418202	Mus muscu
c1490	19	0.8	2655	3	AK039095	AK039095	Mus muscu

1491	19	0.8	2773	3	AK082063	AK082063 Mus muscu
1492	19	0.8	3600	3	AK080619	AK080619 Mus muscu
1493	19	0.8	3694	3	AK032317	AK032317 Mus muscu
1494	19	0.8	4233	3	AK037707	AK037707 Mus muscu
c1495	18	0.8	57	8	AZ755655	AZ755655 ev02f07.x
1496	18	0.8	84	1	AA256701	AA256701 zr83h11.s
c1497	18	0.8	111	8	AZ241770	AZ241770 RPCI-23-8
1498	18	0.8	115	9	CL888966	CL888966 abf93c06.
c1499	18	0.8	136	1	AA780996	AA780996 ah32e01.s
1500	18	0.8	143	5	BQ511622	BQ511622 EST619037

ALIGNMENTS

RESULT 1

AY404343

LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404343

VERSION AY404343.1 GI:39760320

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 48.8%; Score 1131; DB 9; Length 1182;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1418 CCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCAC 1477
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 Db 1081 TTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCT 1140

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RESULT 2
 CN396938

LOCUS CN396938 759 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000417785787 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN396938
 VERSION CN396938.1 GI:47384533
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 759)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J and Stanton, L.W.
 TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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FEATURES
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RESULT 3

BQ216829

LOCUS BQ216829 879 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT_7594754 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6043558
 5', mRNA sequence.

ACCESSION BQ216829

VERSION BQ216829.1 GI:20398229

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 879)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence start: 17

High quality sequence stop: 671.

FEATURES

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Location/Qualifiers

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/db_xref="taxon:9606"

/clone="IMAGE:6043558"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_92"

/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally; oligo-dT primed..

Average insert size 2.5 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

ORIGIN

Query Match 31.2%; Score 725; DB 5; Length 879;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	804	TGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTG	863
Db	25	TGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTG	84
Qy	864	TTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACT	923
Db	85	TTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACT	144
Qy	924	TCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACA	983
Db	145	TCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACA	204
Qy	984	CCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAG	1043
Db	205	CCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAG	264
Qy	1044	GGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG	1103
Db	265	GGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG	324
Qy	1104	TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT	1163
Db	325	TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT	384
Qy	1164	TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG	1223
Db	385	TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG	444
Qy	1224	TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT	1283
Db	445	TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT	504
Qy	1284	TTGGTGTCTTCTATTCAAGTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAC	1343
Db	505	TTGGTGTCTTCTATTCAAGTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAC	564
Qy	1344	AAATCATGGAAGACAAGAGATAACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCT	1403
Db	565	AAATCATGGAAGACAAGAGATAACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCT	624
Qy	1404	CCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAG	1463
Db	625	CCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAG	684
Qy	1464	GGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGT	1523
Db	685	GGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGC	744
Qy	1524	TCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGG	1579
Db	745	TCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGG	800

RESULT 4

CD050395

LOCUS CD050395 916 bp mRNA linear EST 09-MAY-2003

DEFINITION AGENCOURT_13977999 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.

Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
 |||
 Db 294 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 353
 Qy 301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
 |||
 Db 354 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 413
 Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
 |||
 Db 414 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 473
 Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
 |||
 Db 474 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 533
 Qy 481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
 |||
 Db 534 CTTGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 592
 Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
 |||
 Db 593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 652
 Qy 601 AATCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
 |||
 Db 653 AATCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 712
 Qy 661 GGGCCGAGTGAAGAATTTTCTGAT 684
 |||
 Db 713 GGGCCGAGTGAAGAATTTTCTGAT 736

RESULT 5

CN396939

LOCUS CN396939 510 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000599940872 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396939

VERSION CN396939.1 GI:47384534

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 510)

AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
 Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
 Lebkowski,J and Stanton,L.W.

TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@geron.com
Insert Length: 510 Std Error: 0.00.

FEATURES
source Location/Qualifiers
1. .510
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="oligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."

ORIGIN

Query Match 19.7%; Score 457; DB 7; Length 510;
Best Local Similarity 99.8%; Pred. No. 2.3e-232;
Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1109 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTG 1168
          |||
Db      3 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTG 62

Qy      1169 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 1228
          |||
Db      63 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 122

Qy      1229 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 1288
          |||
Db      123 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 182

Qy      1289 GTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 1348
          |||
Db      183 GTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242

Qy      1349 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCAC 1408
          |||
Db      243 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCAC 302

Qy      1409 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 1468
          |||
Db      303 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 362

Qy      1469 GCGACGCACCTCAAGCCCTATGTCTTTTCCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGAC 1528
          |||
Db      363 GCGACGCACCTCAAGCCCTATGTCTTTTCCAGCAGCCCTGGCATGAGCAGTACCTGCTCGAC 422

Qy      1529 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 1588
          |||
Db      423 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 482

Qy      1589 GGCATGGCTGTCTGGTGGCTGCGTGGGG 1616
          |||
Db      483 GGCATGGCTGTCTGGTGGCTGCGTGGGG 510
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RESULT 6

AI917116/c

LOCUS AI917116 430 bp mRNA linear EST 14-DEC-1999

DEFINITION ts52a02.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232170 3', mRNA sequence.

ACCESSION AI917116

VERSION AI917116.1 GI:5636971

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 430)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1614 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 420.

FEATURES Location/Qualifiers

source

1..430

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2232170"

/tissue_type="renal cell tumor"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Kid8"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"

ORIGIN

Query Match 18.5%; Score 430; DB 1; Length 430;

Best Local Similarity 100.0%; Pred. No. 6.5e-218;

Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1887 AAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAG 1946
|||||

Db 430 AAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAG 371

Qy 1947 CCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCC 2006
|||||

Db 370 CCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCC 311

Qy 2007 TCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAA 2066
 |||
 Db 310 TCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAA 251

Qy 2067 CATCCAAGAAAGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCT 2126
 |||
 Db 250 CATCCAAGAAAGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCT 191

Qy 2127 CTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACA 2186
 |||
 Db 190 CTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACA 131

Qy 2187 GGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAG 2246
 |||
 Db 130 GGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAG 71

Qy 2247 GCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTC 2306
 |||
 Db 70 GCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTC 11

Qy 2307 CCCAACCTCA 2316
 |||
 Db 10 CCCAACCTCA 1

RESULT 7

AI580389/c

LOCUS AI580389 422 bp mRNA linear EST 05-APR-1999

DEFINITION tm42f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160807 3', mRNA sequence.

ACCESSION AI580389

VERSION AI580389.1 GI:4564765

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 422)

AUTHORS. NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 386.

FEATURES

source

Location/Qualifiers

1. .422

/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2160807"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "

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ORIGIN

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Query Match          18.2%; Score 422; DB 1; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-213;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1888 AGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGC 1947
        |||
Db      422 AGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGC 363

Qy      1948 CTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCT 2007
        |||
Db      362 CTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCT 303

Qy      2008 CCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTACTATCTATCATGGAATAAC 2067
        |||
Db      302 CCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTACTATCTATCATGGAATAAC 243

Qy      2068 ATCCAAGAAAGACACCTTGCATATTCTTTAGTTTCTGTTTTGTTCTCCACATATTCTC 2127
        |||
Db      242 ATCCAAGAAAGACACCTTGCATATTCTTTAGTTTCTGTTTTGTTCTCCACATATTCTC 183

Qy      2128 TTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAG 2187
        |||
Db      182 TTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAG 123

Qy      2188 GTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGG 2247
        |||
Db      122 GTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGG 63

Qy      2248 CATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCC 2307
        |||
Db      62 CATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCC 3

Qy      2308 CC 2309
        ||
Db      2 CC 1

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RESULT 8
CB158774

LOCUS CB158774 481 bp mRNA linear EST 29-JAN-2003

DEFINITION K-EST0218183 L18POOLln1 Homo sapiens cDNA clone L18POOLln1-14-D07
 5', mRNA sequence.
 ACCESSION CB158774
 VERSION CB158774.1 GI:28143912
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 481)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21c Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 14 row: D column: 07
 High quality sequence stop: 481.
 FEATURES Location/Qualifiers
 source 1. .481
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOLln1-14-D07"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10F"
 /clone_lib="L18POOLln1"
 /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
 Site_2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 6(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 17.0%; Score 395; DB 6; Length 481;
 Best Local Similarity 99.8%; Pred. No. 3.6e-199;
 Matches 445; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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... Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      36 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 95

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db      96 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 155

Qy      121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db      156 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGATGCCATTATCTACT 215
  
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Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
 |||
 Db 216 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 275

Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
 |||
 Db 276 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 335

Qy 301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
 |||
 Db 336 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 395

Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
 |||
 Db 396 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 455

Qy 421 GTTGCACTGCAGTCATTTTTTAAATA 446
 |||
 Db 456 GTTGCACTGCAGTCATTTTTTAAATA 481

RESULT 9

AA633698/c

LOCUS AA633698 439 bp mRNA linear EST 09-MAR-1998
 DEFINITION ag87a11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
 IMAGE:1141436 3', mRNA sequence.

ACCESSION AA633698

VERSION AA633698.1 GI:2556912

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 439)

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
 Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
 Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

TITLE WashU-NCI human EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1564 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 399.

FEATURES

source

Location/Qualifiers

1. .439

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1141436"

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/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hNT neuron (#937233)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

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ORIGIN

```

Query Match          16.1%; Score 373; DB 1; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.2e-187;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1876 TTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCT 1935
          |||
Db      439 TTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCT 380

Qy      1936 CAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGA 1995
          |||
Db      379 CAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGA 320

Qy      1996 CTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTACTATCTA 2055
          |||
Db      319 CTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTACTATCTA 260

Qy      2056 TCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTAGTTTCTGTTTTGTTCTC 2115
          |||
Db      259 TCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTAGTTTCTGTTTTGTTCTC 200

Qy      2116 CCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGAC 2175
          |||
Db      199 CCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGAC 140

Qy      2176 ACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCT 2235
          |||
Db      139 ACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCT 80

Qy      2236 TGGCTGAGCAGGC 2248
          |||
Db      79 TGGCTGAGCAGGC 67

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RESULT 10

BI827790

LOCUS BI827790 901 bp mRNA linear EST 04-OCT-2001

DEFINITION 603075472F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167360 5', mRNA sequence.

ACCESSION BI827790

VERSION BI827790.1 GI:15939340

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 901)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11415 row: p column: 17
 High quality sequence stop: 418.

FEATURES Location/Qualifiers
 source 1. .901
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5167360"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 14.9%; Score 345; DB 4; Length 901;
 Best Local Similarity 99.7%; Pred. No. 2.3e-172;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	24	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	83
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	84	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	143
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	144	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	203
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	204	TTCTGTTTTGTTCTCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	263
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	264	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	323

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 |||
 Db 324 CAGTGAGCTCCTTCTTGGCTGAGCAGGCTTGGAGACTGTAGGTTTCCAGATTTCTGAAA 383
 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCAACCTCA 2316
 |||
 Db 384 AATAAAAGTTTACAGCGTTATCTCTCCCAACCTCA 419

RESULT 11
 BX109306/c

LOCUS BX109306 462 bp mRNA linear EST 07-FEB-2003
 DEFINITION BX109306 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGp998E035522 ;
 IMAGE:2232170, mRNA sequence.
 ACCESSION BX109306
 VERSION BX109306.1 GI:27835717
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 462)
 AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.
 TITLE Human UnigeneSet - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGp998E035522.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human UnigeneSet - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13u, Primer sequence: CGTTGTAAACGACGGCCAGT.

FEATURES Location/Qualifiers
 source 1. .462
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGp998E035522 ; IMAGE:2232170"
 /tissue_type="renal cell tumor"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Kid8"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"

ORIGIN

Query Match 14.1%; Score 328; DB 5; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.7e-163;
Matches 448; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1869 CCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCAC 1928
          |||
Db      462 CCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCAC 403

Qy      1929 TGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCAC 1988
          |||
Db      402 TGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCAC 343

Qy      1989 ACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTA 2048
          |||
Db      342 ACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCTA 283

Qy      2049 CTATCTATCATGGAATAACATCC-AAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTT 2107
          |||
Db      282 CTATCTATCATGGAATAACATCCAAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTT 223

Qy      2108 TTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAG 2167
          |||
Db      222 TTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAG 163

Qy      2168 GGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAG 2227
          |||
Db      162 GGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAG 103

Qy      2228 CTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAAAATAAAA 2287
          |||
Db      102 CTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAAAATAAAA 43

Qy      2288 GTTTACAGCGTTATCTCTCCCCAACCTCA 2316
          |||
Db      42 GTTTACAGCGTTATCTCTCCCCAACCTCA 14
```

RESULT 12

BP431975

LOCUS BP431975 360 bp mRNA linear EST 09-SEP-2003

DEFINITION BP431975 leukemia cell normalized cDNA library Homo sapiens cDNA clone LEU2245_30_D1, mRNA sequence.

ACCESSION BP431975

VERSION BP431975.1 GI:34554674

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 360)

AUTHORS Takagaki,K., Katsuma,S., Horio,T., Kaminishi,Y., Hada,Y., Tanaka,T., Ohgi,T. and Yano,J.

TITLE cDNA microarray analysis of altered gene expression in Ara-C-treated leukemia cells

JOURNAL Biochem. Biophys. Res. Commun. 309 (2), 351-358 (2003)

MEDLINE 22831100

PUBMED 12951057
COMMENT Contact: Kazuchika Takagaki
Research Laboratories
Nippon Shinyaku Co. Ltd.
Sakura 3-14-1, Tsukuba, Ibaraki 305-0003, Japan
Tel: 81-29-850-6242
Fax: 81-29-850-6217
Email: k.takagaki@nippon-shinyaku.co.jp.

FEATURES Location/Qualifiers
source 1. .360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LEU2245_30_D1"
/cell_type="leukemia cell"
/clone_lib="leukemia cell normalized cDNA library"
/note="mRNA expressed in leukemia cells (mixture of
CCRF-CEM, K562, HL-60, MOLT-4, or RPMI-8226)"

ORIGIN

Query Match 13.1%; Score 305; DB 5; Length 360;
Best Local Similarity 99.7%; Pred. No. 5.5e-151;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1783 CATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGC 1842
          |||
Db        5 CATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGC 64

Qy      1843 AGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGA 1902
          |||
Db        65 AGAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGA 124

Qy      1903 TTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTT 1962
          |||
Db       125 TTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTT 184

Qy      1963 CCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTA 2022
          |||
Db       185 CCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTA 244

Qy      2023 GTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACAC 2082
          |||
Db       245 GTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACAC 304

Qy      2083 CTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCA 2138
          |||
Db       305 CTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCA 360
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RESULT 13

AI654867/c

LOCUS AI654867 1055 bp mRNA linear EST 17-DEC-1999
DEFINITION wb65c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2310550 3',
mRNA sequence.

ACCESSION AI654867

VERSION AI654867.1 GI:4738846

KEYWORDS EST.

Db 361 GCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAA 302

Qy 1630 GGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTT 1689
 |||

Db 301 GGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTT 242

Qy 1690 CTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTG 1749
 |||

Db 241 CTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTG 182

Qy 1750 TTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1794
 |||

Db 181 TTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 137

RESULT 14

R19994

LOCUS R19994 460 bp mRNA linear EST 17-APR-1995

DEFINITION yg38h02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone

IMAGE:34999 5' similar to SP:UDBX_RABIT P36514

UDP-GLUCURONOSYLTRANSFERASE MICROSOMAL ;, mRNA sequence.

ACCESSION R19994

VERSION R19994.1 GI:774628

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 460)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 3245

High quality sequence stops: 345

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 3245 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 345.

FEATURES

source

Location/Qualifiers

1. .460

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:407351"

/db_xref="taxon:9606"

/clone="IMAGE:34999"

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/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain lNIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AACTGGAAGAATTTCGCGCCGCGCAGGAATTTTTTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

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ORIGIN

```

Query Match          12.5%; Score 290; DB 7; Length 460;
Best Local Similarity 100.0%; Pred. No. 6.1e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1044 GGGTGATATGGAAGTGTCTAGTGTTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAATG 1103
          |||
Db       73 GGGTGATATGGAAGTGTCTAGTGTTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAATG 132

Qy      1104 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 1163
          |||
Db       133 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 192

Qy      1164 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 1223
          |||
Db       193 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 252

Qy      1224 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 1283
          |||
Db       253 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 312

Qy      1284 TTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 1333
          |||
Db       313 TTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 362

```

RESULT 15

BF510946/c

```

LOCUS      BF510946          363 bp    mRNA    linear    EST 06-DEC-2000
DEFINITION UI-H-BI4-apo-g-12-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3088318 3', mRNA sequence.
ACCESSION  BF510946
VERSION    BF510946.1  GI:11594170
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 363)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)

```

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 NCI-CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES Location/Qualifiers
 source 1. .363
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3088318"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_Sub8"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub8
 is a subtracted library derived from NCI_CGAP_Sub5. The
 NCI_CGAP_Sub8 library had 2.5 million recombinants. A
 single-stranded DNA preparation of NCI_CGAP_Sub5 was used
 as a tracer in a subtractive hybridization with a driver
 comprising: a pool of clones from NCI_CGAP_Sub5 (IMAGE
 clone Ids 2732833-2737415, 3068040-3069191; 25% of the
 driver population), a pool of clones from NCI_CGAP_Sub4
 (IMAGE clone Ids 2723592-2729326; 25% of the driver
 population), NCI_CGAP_Sub6 (pool AIF-AJU, IMAGE Ids
 2728969-2733190; 25% of the driver population), and
 NCI_CGAP_Sub7 (IMAGE Ids 3069192-3072238,
 3081864-3084550; 25% of the driver population).
 Subtraction was performed as previously described
 [Bonaldo, Lennon & Soares (1996): Normalization and
 Subtraction: Two Approaches To Facilitate Gene Discovery.
 Genome Research 6, 791-806.
 TAG_TISSUE=germ cell
 TAG_LIB=NCI_CGAP_GC4
 TAG_SEQ=AAATC"

ORIGIN

Query Match 12.3%; Score 286; DB 2; Length 363;
 Best Local Similarity 99.7%; Pred. No. 8.3e-141;
 Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1980	CCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTC	2039
Db	353	CCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTC	294
Qy	2040	CTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAG	2099
Db	293	CTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAG	234
Qy	2100	TTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGA	2159
Db	233	TTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGA	174

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Qy      2160 GAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCC 2219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      173  GAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCC 114

Qy      2220 ACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAA 2279
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      113  ACAGTGAGCTCCTTCTCGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAA 54

Qy      2280 AAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 2316
          ||||||||||||||||||||||||||||||||||||
Db      53  AAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 17

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Search completed: March 25, 2005, 11:50:31
Job time : 6963 secs

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:50:21 ; Search time 9713 Seconds
(without alignments)
11573.778 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccgggcgcc.....tctctccccaacctcactaa 2320

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	2320	100.0	2320	6	AX697213	AX697213 Sequence	
2	2320	100.0	2320	9	AY358416	AY358416 Homo sapi	
3	2162	93.2	2341	6	AX136141	AX136141 Sequence	

	4	2162	93.2	2341	6	BD123523	BD123523	Secretary
	5	2162	93.2	2341	9	AK075383	AK075383	Homo sapi
	6	1957	84.4	2944	6	AX548037	AX548037	Sequence
	7	905	39.0	1836	6	CQ726650	CQ726650	Sequence
c	8	807	34.8	88948	2	AC008947	AC008947	Homo sapi
	9	807	34.8	179513	9	AC016612	AC016612	Homo sapi
	10	776	33.4	2263	6	AX958403	AX958403	Sequence
c	11	536	23.1	148069	2	AC025476	AC025476	Homo sapi
c	12	468	20.2	594	6	AX136632	AX136632	Sequence
c	13	468	20.2	594	6	BD123872	BD123872	Secretary
	14	422	18.2	125145	2	AC022136	AC022136	Homo sapi
	15	230	9.9	2426	6	AR541778	AR541778	Sequence
	16	164	7.1	102255	2	AC026735	AC026735	Homo sapi
	17	156	6.7	88948	2	AC008947	AC008947	Homo sapi
	18	139	6.0	770	6	AX136483	AX136483	Sequence
	19	139	6.0	770	6	BD123723	BD123723	Secretary
	20	68	2.9	1572	6	AX359923	AX359923	Sequence
	21	68	2.9	2082	6	AX359921	AX359921	Sequence
	22	68	2.9	2086	6	AX327327	AX327327	Sequence
	23	68	2.9	2759	9	BC068446	BC068446	Homo sapi
	24	68	2.9	2797	6	AX155211	AX155211	Sequence
	25	68	2.9	2823	6	AX714604	AX714604	Sequence
	26	68	2.9	2823	9	AK057066	AK057066	Homo sapi
	27	68	2.9	3108	9	BC035012	BC035012	Homo sapi
	28	68	2.9	5002	6	CQ842882	CQ842882	Sequence
	29	68	2.9	5002	9	AK125803	AK125803	Homo sapi
	30	68	2.9	105885	9	AC008860	AC008860	Homo sapi
	31	59	2.5	148069	2	AC025476	AC025476	Homo sapi
	32	52	2.2	1842	6	AX747286	AX747286	Sequence
	33	52	2.2	1842	9	AK091977	AK091977	Homo sapi
	34	47	2.0	291	6	CQ740738	CQ740738	Sequence
	35	45	1.9	45	6	AX697217	AX697217	Sequence
c	36	45	1.9	125145	2	AC022136	AC022136	Homo sapi
c	37	30	1.3	165304	9	AC112204	AC112204	Homo sapi
c	38	29	1.2	277	6	CQ350335	CQ350335	Sequence
c	39	29	1.2	507	6	CQ337751	CQ337751	Sequence
	40	26	1.1	2192	10	BC034837	BC034837	Mus muscu
	41	26	1.1	2196	10	BC022134	BC022134	Mus muscu
	42	26	1.1	2210	10	AK128903	AK128903	Mus muscu
	43	26	1.1	2212	6	AX155214	AX155214	Sequence
	44	26	1.1	2228	10	BC025940	BC025940	Mus muscu
	45	26	1.1	156499	2	AC132893	AC132893	Mus muscu
c	46	26	1.1	156499	2	AC132893	AC132893	Mus muscu
	47	26	1.1	170142	9	AP002383	AP002383	Homo sapi
	48	26	1.1	174742	2	AC016896	AC016896	Homo sapi
	49	26	1.1	195466	2	AC032024	AC032024	Homo sapi
	50	26	1.1	251769	2	AC117913	AC117913	Rattus no
c	51	24	1.0	24	6	AX155221	AX155221	Sequence
	52	24	1.0	24	6	AX697215	AX697215	Sequence
c	53	24	1.0	24	6	AX697216	AX697216	Sequence
c	54	23	1.0	23	6	AX697387	AX697387	Sequence
	55	23	1.0	846	6	AR551278	AR551278	Sequence
	56	23	1.0	185771	2	BX510940	BX510940	Danio rer
	57	23	1.0	197225	9	AC093835	AC093835	Homo sapi
c	58	22	0.9	582	6	AR383593	AR383593	Sequence
c	59	22	0.9	582	6	AR383617	AR383617	Sequence
c	60	22	0.9	1706	9	HSU79259	U79259	Human clone

c	61	22	0.9	1707	6	CQ717576	CQ717576 Sequence
c	62	22	0.9	1744	9	BC002677	BC002677 Homo sapi
c	63	22	0.9	1744	9	BC014394	BC014394 Homo sapi
c	64	22	0.9	2661	6	CQ842468	CQ842468 Sequence
c	65	22	0.9	2661	9	AK125431	AK125431 Homo sapi
c	66	22	0.9	6236	6	AX459735	AX459735 Sequence
c	67	22	0.9	125287	9	HS159A19	AL031729 Human DNA
	68	22	0.9	149146	2	AL583851	AL583851 Homo sapi
	69	22	0.9	163233	2	AC123388	AC123388 Rattus no
c	70	22	0.9	167454	2	BX284610	BX284610 Homo sapi
	71	22	0.9	175542	2	AC150062	AC150062 Gallus ga
	72	22	0.9	177909	2	AC031997	AC031997 Homo sapi
	73	22	0.9	201493	9	AL691520	AL691520 Human DNA
	74	22	0.9	213393	2	AL645475	AL645475 Homo sapi
c	75	22	0.9	223443	2	AC112801	AC112801 Rattus no
	76	22	0.9	227099	2	AC130756	AC130756 Rattus no
c	77	22	0.9	242883	2	AC112055	AC112055 Rattus no
c	78	22	0.9	252427	2	AC111287	AC111287 Rattus no
c	79	21	0.9	21	6	AX697386	AX697386 Sequence
	80	21	0.9	32260	10	MMU298076	AJ298076 Mus muscu
c	81	21	0.9	83549	9	AC004752	AC004752 Homo sapi
	82	21	0.9	90450	10	AL627226	AL627226 Mouse DNA
c	83	21	0.9	102807	2	AP000674	AP000674 Homo sapi
	84	21	0.9	104824	9	HS73H22	AL035699 Human DNA
c	85	21	0.9	110000	2	AC091341_6	Continuation (7 of
	86	21	0.9	110000	2	AC117310_0	AC117310 Rattus no
c	87	21	0.9	119419	2	AP000666	AP000666 Homo sapi
c	88	21	0.9	126392	2	AC018785	AC018785 Homo sapi
	89	21	0.9	128422	9	AL357139	AL357139 Human DNA
c	90	21	0.9	131556	2	AC132404	AC132404 Mus muscu
	91	21	0.9	131746	2	AC084842	AC084842 Homo sapi
c	92	21	0.9	139260	9	AC066587	AC066587 Homo sapi
	93	21	0.9	140073	9	CNS01DTO	AL132819 Human chr
c	94	21	0.9	159600	2	AC113296	AC113296 Mus muscu
c	95	21	0.9	160341	9	AL161629	AL161629 Human DNA
c	96	21	0.9	160644	2	AC143585	AC143585 Macaca mu
	97	21	0.9	163569	2	AC023293	AC023293 Homo sapi
	98	21	0.9	164784	2	AP001384	AP001384 Homo sapi
c	99	21	0.9	166065	2	AC149014	AC149014 Papio anu
c	100	21	0.9	166294	2	BX537330	BX537330 Danio rer
c	101	21	0.9	166649	9	AL353633	AL353633 Human DNA
c	102	21	0.9	167470	2	AC136060	AC136060 Rattus no
c	103	21	0.9	167573	10	AC121587	AC121587 Mus muscu
	104	21	0.9	168202	10	AC134826	AC134826 Mus muscu
	105	21	0.9	169978	9	AC017013	AC017013 Homo sapi
c	106	21	0.9	170138	5	BX569781	BX569781 Zebrafish
c	107	21	0.9	172382	2	AC149046	AC149046 Papio anu
c	108	21	0.9	172453	2	AC015889	AC015889 Homo sapi
c	109	21	0.9	172793	2	AC023659	AC023659 Homo sapi
	110	21	0.9	174949	2	AC111342	AC111342 Rattus no
c	111	21	0.9	176766	10	AC113329	AC113329 Mus muscu
	112	21	0.9	179528	9	AC026189	AC026189 Homo sapi
c	113	21	0.9	180081	10	AC122496	AC122496 Mus muscu
	114	21	0.9	181186	2	AC069264	AC069264 Homo sapi
	115	21	0.9	181460	10	AL672181	AL672181 Mouse DNA
	116	21	0.9	184039	9	CNS018OX	AL109767 Human chr
c	117	21	0.9	184509	2	AC113237	AC113237 Canis fam

c 118	21	0.9	188305	10	AC147559	AC147559 Mus muscu
c 119	21	0.9	189995	9	AC018822	AC018822 Homo sapi
120	21	0.9	195873	10	AL805944	AL805944 Mouse DNA
c 121	21	0.9	198652	9	AC009303	AC009303 Homo sapi
c 122	21	0.9	199275	9	AC011401	AC011401 Homo sapi
123	21	0.9	199814	9	AC023480	AC023480 Homo sapi
124	21	0.9	200317	9	HS69B13	AL035698 Human DNA
c 125	21	0.9	200655	9	AC091825	AC091825 Homo sapi
126	21	0.9	202052	2	AC084827	AC084827 Mus muscu
127	21	0.9	202587	2	AC119862	AC119862 Mus muscu
c 128	21	0.9	205183	2	AC093355	AC093355 Mus muscu
c 129	21	0.9	207974	10	AL831771	AL831771 Mouse DNA
130	21	0.9	211973	2	AP001163	AP001163 Homo sapi
c 131	21	0.9	221535	9	AP001359	AP001359 Homo sapi
c 132	21	0.9	222856	2	AC128437	AC128437 Rattus no
c 133	21	0.9	225611	2	AC149606	AC149606 Mus muscu
c 134	21	0.9	230525	2	AC096982	AC096982 Rattus no
135	21	0.9	234360	2	AC118763	AC118763 Rattus no
136	21	0.9	239559	2	AC095531	AC095531 Rattus no
c 137	21	0.9	242227	10	AC124120	AC124120 Mus muscu
138	21	0.9	252520	2	AC131432	AC131432 Rattus no
139	21	0.9	252625	2	AC130076	AC130076 Rattus no
c 140	21	0.9	253026	2	AC098084	AC098084 Rattus no
c 141	21	0.9	254828	2	AC111760	AC111760 Rattus no
c 142	21	0.9	261672	2	AC111815	AC111815 Rattus no
143	21	0.9	263236	2	AC094070	AC094070 Rattus no
c 144	21	0.9	264264	2	AC094210	AC094210 Rattus no
c 145	21	0.9	270063	10	AC117635	AC117635 Mus muscu
146	21	0.9	275392	2	AC095297	AC095297 Rattus no
c 147	21	0.9	279589	2	AC073768	AC073768 Mus muscu
148	21	0.9	291856	2	AC119388	AC119388 Rattus no
149	21	0.9	294316	2	AC131613	AC131613 Rattus no
c 150	21	0.9	323764	2	BX511194	BX511194 Danio rer
c 151	21	0.9	344000	1	TACID1	AL445063 Thermopla
152	21	0.9	349391	1	BX572095	BX572095 Prochloro
153	20	0.9	298	6	CQ741582	CQ741582 Sequence
154	20	0.9	464	11	G60984	G60984 SHGC-84035
c 155	20	0.9	513	14	CHDNAMGG	X89243 Canine herp
c 156	20	0.9	573	14	AY373026	AY373026 Bean yell
c 157	20	0.9	573	14	AY376313	AY376313 Bean yell
158	20	0.9	582	11	G97497	G97497 S208P6362RD
159	20	0.9	669	9	HSA338450	AJ338450 Homo sapi
160	20	0.9	739	11	BV037877	BV037877 S212P6686
161	20	0.9	1742	3	AB072589	AB072589 Bombyx mo
162	20	0.9	2677	9	BC025385	BC025385 Homo sapi
163	20	0.9	2870	5	BC084686	BC084686 Danio rer
164	20	0.9	3673	8	ATPHYE	X76610 A.thaliana
c 165	20	0.9	32538	3	CEZK829	Z73899 Caenorhabdi
166	20	0.9	40873	2	CEH04I09	Z92848 Caenorhabdi
167	20	0.9	41330	3	CBRG35F02	AC084556 Caenorhab
c 168	20	0.9	42141	3	CEY54G9A	AL032648 Caenorhab
169	20	0.9	47081	3	CEUNC22	X15423 Caenorhabdi
c 170	20	0.9	47417	2	AC100702	AC100702 Mus muscu
c 171	20	0.9	48022	9	AC116617	AC116617 Homo sapi
172	20	0.9	54962	3	CELTWIMUSC	L10351 Caenorhabdi
173	20	0.9	55379	2	AC083988	AC083988 Homo sapi
c 174	20	0.9	57655	2	AC100690	AC100690 Mus muscu

c 175	20	0.9	58427	8	ATF15J5	AL110123 Arabidops
c 176	20	0.9	62708	2	AC097780_3	Continuation (4 of
c 177	20	0.9	63015	10	AL732310	AL732310 Mouse DNA
178	20	0.9	67061	9	HSDJ306F2	AL121573 Human DNA
c 179	20	0.9	68673	2	AC124071	AC124071 Homo sapi
180	20	0.9	69158	2	AC107955	AC107955 Homo sapi
c 181	20	0.9	69158	2	AC107955	AC107955 Homo sapi
c 182	20	0.9	80355	2	AC016505	AC016505 Homo sapi
c 183	20	0.9	81099	9	AC110770	AC110770 Homo sapi
184	20	0.9	84224	9	AL358978	AL358978 Human DNA
c 185	20	0.9	87849	3	AC084453	AC084453 Caenorhab
186	20	0.9	90775	2	AC074396	AC074396 Homo sapi
c 187	20	0.9	91822	9	AC122697	AC122697 Homo sapi
188	20	0.9	92439	2	AC101765	AC101765 Mus muscu
c 189	20	0.9	94529	6	AX695977	AX695977 Sequence
190	20	0.9	94977	2	AC139987	AC139987 Rattus no
191	20	0.9	96512	9	AC022539	AC022539 Homo sapi
c 192	20	0.9	99892	5	BX323581	BX323581 Zebrafish
193	20	0.9	104281	8	AC129092	AC129092 Medicago
c 194	20	0.9	106525	9	AC068641	AC068641 Homo sapi
c 195	20	0.9	106724	10	AF130357	AF130357 Mus muscu
c 196	20	0.9	107514	2	AC026404	AC026404 Homo sapi
197	20	0.9	109075	5	AY739095	AY739095 Takifugu
c 198	20	0.9	110000	2	AC106549_0	AC106549 Rattus no
c 199	20	0.9	110000	2	AC106549_1	Continuation (2 of
200	20	0.9	110000	2	AC119467_0	AC119467 Rattus no
c 201	20	0.9	110000	2	AC151831_1	Continuation (2 of
c 202	20	0.9	110000	2	AC151831_2	Continuation (3 of
203	20	0.9	110000	2	CR555291_3	Continuation (4 of
204	20	0.9	110000	2	AC073860_2	Continuation (3 of
c 205	20	0.9	112010	2	AC010302	AC010302 Homo sapi
c 206	20	0.9	112978	9	AC022139	AC022139 Homo sapi
c 207	20	0.9	114290	9	AL138814	AL138814 Human DNA
c 208	20	0.9	114873	10	AC124211	AC124211 Mus muscu
c 209	20	0.9	115293	9	AC127460	AC127460 Homo sapi
210	20	0.9	115372	9	AL359202	AL359202 Human DNA
c 211	20	0.9	115399	2	AP004322	AP004322 Oryza sat
212	20	0.9	116871	2	AL138738	AL138738 Homo sapi
213	20	0.9	118787	10	AL844486	AL844486 Mouse DNA
214	20	0.9	120492	9	AC092580	AC092580 Homo sapi
c 215	20	0.9	121720	8	AC021044	AC021044 Arabidops
216	20	0.9	125507	9	AL450336	AL450336 Human DNA
217	20	0.9	126360	2	AC117274	AC117274 Bos tauru
218	20	0.9	128739	8	AP004741	AP004741 Oryza sat
219	20	0.9	131757	9	AC004540	AC004540 Homo sapi
c 220	20	0.9	133225	9	AC108089	AC108089 Homo sapi
221	20	0.9	135473	10	AC102705	AC102705 Mus muscu
c 222	20	0.9	137302	4	AY386695	AY386695 Oryctolag
223	20	0.9	138121	9	AC025431	AC025431 Homo sapi
c 224	20	0.9	138173	2	AC151513	AC151513 Dasypus n
c 225	20	0.9	139446	4	AY386697	AY386697 Oryctolag
c 226	20	0.9	140023	2	AC151646	AC151646 Dasypus n
c 227	20	0.9	140385	9	HS20B11	AL031770 Human DNA
228	20	0.9	142837	2	AC113232	AC113232 Canis fam
229	20	0.9	142867	9	AC091184	AC091184 Homo sapi
c 230	20	0.9	143118	2	AC079348	AC079348 Homo sapi
c 231	20	0.9	144652	2	CR388085	CR388085 Danio rer

c 232	20	0.9	145383	2	AC116816	AC116816	Mus muscu
233	20	0.9	145564	5	AL929247	AL929247	Zebrafish
234	20	0.9	147724	8	AP003525	AP003525	Oryza sat
c 235	20	0.9	149902	2	AC110667	AC110667	Canis fam
236	20	0.9	151595	5	AL954191	AL954191	Zebrafish
237	20	0.9	153134	5	BX663506	BX663506	Zebrafish
c 238	20	0.9	154359	2	AC021718	AC021718	Homo sapi
c 239	20	0.9	154821	8	AP003709	AP003709	Oryza sat
c 240	20	0.9	154864	9	AC008070	AC008070	Homo sapi
c 241	20	0.9	155010	2	CR524821	CR524821	Danio rer
242	20	0.9	155332	9	AC109581	AC109581	Homo sapi
243	20	0.9	156857	2	BX537298	BX537298	Mus muscu
244	20	0.9	158093	9	AL390123	AL390123	Human DNA
c 245	20	0.9	159620	9	AL354835	AL354835	Human DNA
246	20	0.9	160513	2	AC113563	AC113563	Canis fam
c 247	20	0.9	161674	10	AL807394	AL807394	Mouse DNA
c 248	20	0.9	161891	2	AC141360	AC141360	Sus scrof
c 249	20	0.9	161892	2	AC123875	AC123875	Mus muscu
250	20	0.9	163243	9	AL513304	AL513304	Human DNA
251	20	0.9	163688	2	AC148274	AC148274	Macropus
c 252	20	0.9	163861	9	AL356772	AL356772	Human DNA
c 253	20	0.9	164642	2	AC096873	AC096873	Rattus no
254	20	0.9	164706	9	AC068614	AC068614	Homo sapi
c 255	20	0.9	164711	9	BS000216	BS000216	Pan trogl
256	20	0.9	165036	9	AC133010	AC133010	Homo sapi
c 257	20	0.9	166600	9	AL391121	AL391121	Human DNA
c 258	20	0.9	166698	2	AC025158	AC025158	Homo sapi
c 259	20	0.9	167120	10	AC110178	AC110178	Mus muscu
c 260	20	0.9	167281	2	AP001147	AP001147	Homo sapi
261	20	0.9	167874	10	BX950219	BX950219	Mouse DNA
262	20	0.9	168544	9	AL513307	AL513307	Human DNA
c 263	20	0.9	170028	2	AP002435	AP002435	Homo sapi
c 264	20	0.9	170118	9	AC012384	AC012384	Homo sapi
c 265	20	0.9	171474	2	AC135752	AC135752	Rattus no
c 266	20	0.9	171742	5	CR388178	CR388178	Zebrafish
267	20	0.9	171791	2	CR847938	CR847938	Danio rer
c 268	20	0.9	171850	2	AC102284	AC102284	Mus muscu
c 269	20	0.9	172460	2	AC079798	AC079798	Homo sapi
270	20	0.9	172902	2	AL358816	AL358816	Homo sapi
271	20	0.9	173277	2	AC148175	AC148175	Mus muscu
c 272	20	0.9	173641	2	AC141089	AC141089	Rattus no
273	20	0.9	174256	2	AC022572	AC022572	Homo sapi
c 274	20	0.9	174548	9	AP002342	AP002342	Homo sapi
c 275	20	0.9	174712	10	AL831725	AL831725	Mouse DNA
276	20	0.9	176080	2	AC118314	AC118314	Rattus no
277	20	0.9	176268	2	AL591001	AL591001	Homo sapi
c 278	20	0.9	176304	2	AC102182	AC102182	Mus muscu
c 279	20	0.9	176344	2	AC023117	AC023117	Homo sapi
280	20	0.9	177879	2	AC087822	AC087822	Homo sapi
281	20	0.9	179668	2	CR626936	CR626936	Danio rer
c 282	20	0.9	179686	2	AC023987	AC023987	Homo sapi
283	20	0.9	180000	2	AC006394	AC006394	Homo sapi
c 284	20	0.9	180633	2	AC080056	AC080056	Homo sapi
c 285	20	0.9	180652	2	CR762436	CR762436	Danio rer
286	20	0.9	182250	2	AC139988	AC139988	Rattus no
287	20	0.9	182411	9	AC068044	AC068044	Homo sapi
c 288	20	0.9	183460	9	AL356753	AL356753	Human DNA

c 289	20	0.9	183905	2	CR847569	CR847569	Danio rer
c 290	20	0.9	184037	9	CNS01RIM	AL163642	Human chr
291	20	0.9	184583	2	AC079104	AC079104	Homo sapi
c 292	20	0.9	184660	2	BX323862	BX323862	Danio rer
293	20	0.9	184794	2	AP000849	AP000849	Homo sapi
294	20	0.9	185375	2	AC108789	AC108789	Mus muscu
c 295	20	0.9	186930	9	AP001604	AP001604	Homo sapi
296	20	0.9	187614	2	AC115839	AC115839	Mus muscu
297	20	0.9	188890	2	CR628370	CR628370	Danio rer
298	20	0.9	188928	10	AC144630	AC144630	Mus muscu
c 299	20	0.9	189442	10	AC119382	AC119382	Rattus no
c 300	20	0.9	189616	10	AC124480	AC124480	Mus muscu
301	20	0.9	191120	2	AC148124	AC148124	Otolemur
c 302	20	0.9	191448	2	AC124634	AC124634	Mus muscu
303	20	0.9	191927	2	AC109884	AC109884	Rattus no
c 304	20	0.9	192042	9	AC079955	AC079955	Homo sapi
c 305	20	0.9	193483	9	AL356257	AL356257	Human DNA
306	20	0.9	193960	2	AC018905	AC018905	Homo sapi
307	20	0.9	194053	2	AC119434	AC119434	Mus muscu
308	20	0.9	194104	10	AC124510	AC124510	Mus muscu
c 309	20	0.9	194143	8	ATCHRIV48	AL161548	Arabidops
c 310	20	0.9	194827	2	BX294106	BX294106	Danio rer
c 311	20	0.9	195449	10	AC133510	AC133510	Mus muscu
c 312	20	0.9	195466	2	AC032024	AC032024	Homo sapi
313	20	0.9	195549	2	AC151860	AC151860	Bos tauru
314	20	0.9	198197	2	BX322641	BX322641	Mus muscu
315	20	0.9	198197	10	AC125035	AC125035	Mus muscu
316	20	0.9	198831	10	AC122355	AC122355	Mus muscu
c 317	20	0.9	200153	2	AC116759	AC116759	Mus muscu
c 318	20	0.9	200856	5	BX248239	BX248239	Zebrafish
319	20	0.9	201197	9	HS1091N2	AL590764	Homo sapi
c 320	20	0.9	204646	2	AC121130	AC121130	Mus muscu
321	20	0.9	206291	2	AC069188	AC069188	Homo sapi
c 322	20	0.9	207818	2	AC137432	AC137432	Rattus no
323	20	0.9	210915	2	AC116469	AC116469	Mus muscu
c 324	20	0.9	211094	5	BX005335	BX005335	Zebrafish
c 325	20	0.9	211178	10	AC139209	AC139209	Mus muscu
c 326	20	0.9	211743	2	AC136147	AC136147	Mus muscu
c 327	20	0.9	211799	2	AC138229	AC138229	Mus muscu
328	20	0.9	212186	10	AC132237	AC132237	Mus muscu
c 329	20	0.9	212883	2	AC068832	AC068832	Homo sapi
330	20	0.9	213153	2	AC129348	AC129348	Rattus no
c 331	20	0.9	213869	2	AC127959	AC127959	Rattus no
c 332	20	0.9	214756	2	AC119367	AC119367	Rattus no
333	20	0.9	214868	2	AC139122	AC139122	Rattus no
c 334	20	0.9	216615	10	AC107850	AC107850	Mus muscu
c 335	20	0.9	219944	2	AC106194	AC106194	Rattus no
c 336	20	0.9	220558	2	AC096523	AC096523	Rattus no
337	20	0.9	223337	10	AL928564	AL928564	Mouse DNA
338	20	0.9	223367	9	AC018686	AC018686	Homo sapi
339	20	0.9	224386	2	AC099090	AC099090	Rattus no
340	20	0.9	224445	2	AC098492	AC098492	Rattus no
341	20	0.9	225665	2	AC098177	AC098177	Rattus no
c 342	20	0.9	225803	2	AC123641	AC123641	Mus muscu
c 343	20	0.9	226433	2	AC109076	AC109076	Rattus no
c 344	20	0.9	226904	2	AC111606	AC111606	Rattus no
345	20	0.9	227759	2	AC094147	AC094147	Rattus no

346	20	0.9	229425	2	AC126965	AC126965	Rattus no
c 347	20	0.9	230097	2	AC103195	AC103195	Rattus no
c 348	20	0.9	230765	2	AC140337	AC140337	Mus muscu
c 349	20	0.9	233527	2	AC128398	AC128398	Rattus no
c 350	20	0.9	233619	2	AC128426	AC128426	Rattus no
c 351	20	0.9	234771	2	AC105616	AC105616	Rattus no
352	20	0.9	235045	2	AC119588	AC119588	Rattus no
c 353	20	0.9	235363	10	AC022062	AC022062	Mus muscu
c 354	20	0.9	235977	2	AC111800	AC111800	Rattus no
c 355	20	0.9	236764	2	AC114057	AC114057	Rattus no
356	20	0.9	237258	2	AC124867	AC124867	Rattus no
357	20	0.9	237581	2	AC098349	AC098349	Rattus no
c 358	20	0.9	238427	2	AC113234	AC113234	Canis fam
359	20	0.9	238831	2	AC107158	AC107158	Rattus no
c 360	20	0.9	239657	2	AC096455	AC096455	Rattus no
c 361	20	0.9	240307	2	AC128067	AC128067	Rattus no
c 362	20	0.9	240597	2	AC094512	AC094512	Rattus no
363	20	0.9	241004	2	AC113922	AC113922	Rattus no
c 364	20	0.9	242036	2	AC126481	AC126481	Rattus no
c 365	20	0.9	242224	2	BX936445	BX936445	Danio rer
366	20	0.9	243863	2	AC137319	AC137319	Rattus no
c 367	20	0.9	246163	2	AC121406	AC121406	Rattus no
c 368	20	0.9	246387	2	AC109737	AC109737	Rattus no
369	20	0.9	248569	2	AC111477	AC111477	Rattus no
370	20	0.9	250492	2	AC137179	AC137179	Rattus no
c 371	20	0.9	250902	2	AC131965	AC131965	Rattus no
c 372	20	0.9	252779	2	AC114107	AC114107	Rattus no
c 373	20	0.9	253169	2	AC094461	AC094461	Rattus no
c 374	20	0.9	253613	2	AC122764	AC122764	Mus muscu
375	20	0.9	253877	2	AC106328	AC106328	Rattus no
376	20	0.9	254280	2	AC131372	AC131372	Rattus no
c 377	20	0.9	256058	2	AC111032	AC111032	Mus muscu
378	20	0.9	258795	2	AC123358	AC123358	Rattus no
379	20	0.9	259608	2	AC123181	AC123181	Rattus no
380	20	0.9	261792	2	AC114707	AC114707	Rattus no
c 381	20	0.9	262967	2	AC110392	AC110392	Rattus no
c 382	20	0.9	263371	2	AC098454	AC098454	Rattus no
383	20	0.9	265382	2	AC114439	AC114439	Rattus no
384	20	0.9	278103	2	AC115418	AC115418	Rattus no
c 385	20	0.9	287188	2	AC091344	AC091344	Rattus no
386	20	0.9	288383	2	AC109947	AC109947	Rattus no
c 387	20	0.9	310985	2	AC130582	AC130582	Rattus no
c 388	20	0.9	315291	2	AC134095	AC134095	Rattus no
c 389	20	0.9	340000	9	AP001699	AP001699	Homo sapi
c 390	20	0.9	340623	2	AC109956	AC109956	Rattus no
391	20	0.9	345588	2	AC119362	AC119362	Rattus no
392	20	0.9	348505	1	BX571870	BX571870	Photorhab
393	20	0.9	349505	2	AC130443	AC130443	Rattus no
c 394	20	0.9	349980	6	CQ870479	CQ870479	Sequence
c 395	20	0.9	349980	6	AX770909	AX770909	Sequence
c 396	19	0.8	165	8	AJ838560	AJ838560	Arabidops
397	19	0.8	282	11	HSU30330	U30330	Human seque
c 398	19	0.8	371	11	BV091192	BV091192	RPAMMSEQ0
399	19	0.8	376	11	G03350	G03350	human STS W
400	19	0.8	500	5	SSDYST2	AF137106	Sargocent
c 401	19	0.8	561	11	G77656	G77656	S210P6090RG
402	19	0.8	597	11	BV044600	BV044600	S212P6382

c 403	19	0.8	607	11	BV026830	BV026830 S209P6252
404	19	0.8	665	4	AY356106	AY356106 Canis fam
c 405	19	0.8	674	6	CQ432519	CQ432519 Sequence
406	19	0.8	719	6	AX067392	AX067392 Sequence
c 407	19	0.8	773	11	BV038537	BV038537 S212P6014
408	19	0.8	834	4	AY355792	AY355792 Canis fam
409	19	0.8	873	6	AX347498	AX347498 Sequence
410	19	0.8	938	9	AK130214	AK130214 Homo sapi
411	19	0.8	1144	8	BOBOPC5	X96408 B.oleracea
c 412	19	0.8	1218	6	AX570443	AX570443 Sequence
413	19	0.8	1371	8	BOBOPC3	X96407 B.oleracea
c 414	19	0.8	1383	6	CQ741637	CQ741637 Sequence
415	19	0.8	1441	8	BOBOCP4	X96409 B.oleracea
416	19	0.8	1662	6	CQ742010	CQ742010 Sequence
c 417	19	0.8	1856	6	AX509814	AX509814 Sequence
418	19	0.8	1933	9	AK130038	AK130038 Homo sapi
c 419	19	0.8	2000	6	AX508065	AX508065 Sequence
420	19	0.8	2023	10	MMU10484	U10484 Mus musculu
421	19	0.8	2024	9	HSA549090	AJ549090 Homo sapi
c 422	19	0.8	2103	8	AF105425	AF105425 Cynodon d
c 423	19	0.8	2206	6	BD209990	BD209990 Human tra
424	19	0.8	2208	8	BOGBOCP4	X96410 B.oleracea
425	19	0.8	2241	9	AY167927	AY167927 Homo sapi
426	19	0.8	2263	10	BC052909	BC052909 Mus muscu
c 427	19	0.8	2309	6	BD157048	BD157048 Primer fo
c 428	19	0.8	2309	6	AX878147	AX878147 Sequence
c 429	19	0.8	2309	9	AK002085	AK002085 Homo sapi
c 430	19	0.8	2318	10	AF480164	AF480164 Mus muscu
c 431	19	0.8	2371	9	AF480163	AF480163 Homo sapi
432	19	0.8	2406	9	HSA549088	AJ549088 Homo sapi
433	19	0.8	2421	9	AY167926	AY167926 Homo sapi
434	19	0.8	2424	6	AX528390	AX528390 Sequence
435	19	0.8	2424	9	HSA549089	AJ549089 Homo sapi
436	19	0.8	2538	6	CQ730160	CQ730160 Sequence
437	19	0.8	2589	9	HSA272034	AJ272034 Homo sapi
438	19	0.8	2589	9	HSA421783	AJ421783 Homo sapi
439	19	0.8	2627	9	BC013947	BC013947 Homo sapi
c 440	19	0.8	2699	6	AR342388	AR342388 Sequence
c 441	19	0.8	2699	6	BD082295	BD082295 76 kDa, 3
442	19	0.8	2714	10	BC060057	BC060057 Mus muscu
443	19	0.8	2714	10	BC060243	BC060243 Mus muscu
444	19	0.8	2724	6	AX347496	AX347496 Sequence
c 445	19	0.8	2798	6	AR342387	AR342387 Sequence
c 446	19	0.8	2798	6	BD082294	BD082294 76 kDa, 3
447	19	0.8	2830	9	BC064390	BC064390 Homo sapi
c 448	19	0.8	2899	9	BC038424	BC038424 Homo sapi
449	19	0.8	2954	6	CQ842138	CQ842138 Sequence
450	19	0.8	2954	9	AK125168	AK125168 Homo sapi
451	19	0.8	3195	10	AF190645	AF190645 Mus muscu
452	19	0.8	3336	10	AF139923	AF139923 Mus muscu
453	19	0.8	3550	6	BD190797	BD190797 Secreted
454	19	0.8	3550	6	AX099520	AX099520 Sequence
c 455	19	0.8	3576	9	HSM806018	BX537516 Homo sapi
c 456	19	0.8	3810	9	HSM803390	AL832083 Homo sapi
c 457	19	0.8	4024	4	AF181119	AF181119 Sus scrof
458	19	0.8	4068	3	AY280698	AY280698 Schistost
c 459	19	0.8	4127	3	AB032259	AB032259 Asterina

c 460	19	0.8	4158	9	HSM805995	BX537514	Homo sapi
461	19	0.8	4283	9	AB020648	AB020648	Homo sapi
462	19	0.8	4352	6	AR339064	AR339064	Sequence
463	19	0.8	4597	10	RNO237670	AJ237670	Rattus no
464	19	0.8	5205	2	AC018203	AC018203	Drosophil
465	19	0.8	5947	3	PFSC04066	AL010241	Plasmodiu
466	19	0.8	6875	8	AB028236	AB028236	Tricholom
c 467	19	0.8	8301	9	AC007456	AC007456	Homo sapi
468	19	0.8	8388	9	HS17CTNS1	AF112441	Homo sapi
469	19	0.8	9171	1	AE007469	AE007469	Streptoco
470	19	0.8	9974	1	AE000629	AE000629	Helicobac
471	19	0.8	10419	8	AB027513	AB027513	Tricholom
472	19	0.8	10749	1	AE013819	AE013819	Yersinia
473	19	0.8	10797	1	AE004396	AE004396	Vibrio ch
c 474	19	0.8	11004	1	AE001150	AE001150	Borrelia
475	19	0.8	11258	1	AE000549	AE000549	Helicobac
476	19	0.8	11447	1	AE000599	AE000599	Helicobac
477	19	0.8	12507	1	AE011843	AE011843	Xanthomon
c 478	19	0.8	12973	2	AC013026	AC013026	Drosophil
479	19	0.8	13206	2	AC014437	AC014437	Drosophil
c 480	19	0.8	14382	10	MMU50715	U50715	Mus musculu
481	19	0.8	14506	1	AE005730	AE005730	Caulobact
482	19	0.8	20543	8	AY028608	AY028608	Brassica
c 483	19	0.8	20549	2	AC068540	AC068540	Homo sapi
c 484	19	0.8	32551	3	CEC26D10	Z54327	Caenorhabdi
c 485	19	0.8	32768	6	CQ788980	CQ788980	Sequence
c 486	19	0.8	32768	6	AR218839	AR218839	Sequence
c 487	19	0.8	32768	6	BD003751	BD003751	Polynucle
488	19	0.8	36298	3	U64842	U64842	Caenorhabdi
489	19	0.8	36371	9	AC097643	AC097643	Homo sapi
490	19	0.8	36428	9	AC110000	AC110000	Homo sapi
491	19	0.8	37010	3	CBRG28M15	AC084544	Caenorhab
492	19	0.8	37968	9	AC120115	AC120115	Homo sapi
c 493	19	0.8	39177	3	CEAC8	Z83097	Caenorhabdi
c 494	19	0.8	39329	9	AC004091	AC004091	Human Cos
c 495	19	0.8	39567	2	AC015562	AC015562	Homo sapi
c 496	19	0.8	39780	2	AC014011	AC014011	Drosophil
497	19	0.8	41367	9	HSU163D10	Z68326	Human DNA s
c 498	19	0.8	41585	9	HSAC000374	AC000374	Human cos
c 499	19	0.8	42081	9	AC005494	AC005494	Homo sapi
c 500	19	0.8	42184	9	AC003068	AC003068	Human Cos
c 501	19	0.8	42296	8	AY459337	AY459337	Oryza sat
502	19	0.8	42432	9	CR589904	CR589904	Human DNA
503	19	0.8	43834	3	AF045643	AF045643	Caenorhab
504	19	0.8	44008	9	AC097644	AC097644	Homo sapi
505	19	0.8	44838	9	AC097642	AC097642	Homo sapi
c 506	19	0.8	44983	9	AL606913	AL606913	Human DNA
c 507	19	0.8	45976	9	AC091868	AC091868	Homo sapi
c 508	19	0.8	46530	2	BX293554_5	Continuation (6 of	
509	19	0.8	49297	9	AC063980	AC063980	Homo sapi
510	19	0.8	50000	6	AR211704	AR211704	Sequence
511	19	0.8	50913	7	AY129332	AY129332	Mycobacte
512	19	0.8	53439	2	AC140621	AC140621	Macaca mu
c 513	19	0.8	55568	2	AC015850_3	Continuation (4 of	
c 514	19	0.8	56168	2	AC101339	AC101339	Mus muscu
c 515	19	0.8	57571	2	AC018724_3	Continuation (4 of	
516	19	0.8	57671	2	AC117828	AC117828	Mus muscu

517	19	0.8	58689	2	AC136343	AC136343 Homo sapi
518	19	0.8	59777	3	AC084454	AC084454 Caenorhab
c 519	19	0.8	60406	9	AL590550	AL590550 Human DNA
c 520	19	0.8	60597	9	AC113611	AC113611 Homo sapi
c 521	19	0.8	62309	9	AC110495	AC110495 Homo sapi
522	19	0.8	62677	2	AC100559	AC100559 Mus muscu
523	19	0.8	62999	2	AC087594	AC087594 Homo sapi
524	19	0.8	63238	2	AC137863	AC137863 Mus muscu
525	19	0.8	64232	2	AC101806	AC101806 Mus muscu
526	19	0.8	64601	9	AC009730	AC009730 Homo sapi
c 527	19	0.8	67220	2	AC022745	AC022745 Mus muscu
c 528	19	0.8	67468	2	AC139148	AC139148 Homo sapi
529	19	0.8	67870	2	AC083787	AC083787 Homo sapi
c 530	19	0.8	67996	2	AC138912	AC138912 Homo sapi
531	19	0.8	68222	9	AL391904	AL391904 Human DNA
c 532	19	0.8	69025	2	AC111171	AC111171 Homo sapi
c 533	19	0.8	69971	9	BX546457	BX546457 Human DNA
534	19	0.8	70991	10	AY225417	AY225417 Mus muscu
c 535	19	0.8	71151	2	AC128128_3	Continuation (4 of
c 536	19	0.8	72351	2	AC100079	AC100079 Mus muscu
537	19	0.8	73778	2	AC090743	AC090743 Homo sapi
c 538	19	0.8	73778	2	AC090743	AC090743 Homo sapi
539	19	0.8	73842	2	AC025657	AC025657 Homo sapi
c 540	19	0.8	74135	2	AC141777	AC141777 Apis mell
541	19	0.8	75803	8	AB016890	AB016890 Arabidops
c 542	19	0.8	76196	1	AY354515	AY354515 Streptomy
543	19	0.8	76746	2	AC139032	AC139032 Homo sapi
544	19	0.8	77127	9	AC104065	AC104065 Homo sapi
c 545	19	0.8	78346	12	AY350710	AY350710 Brassica
c 546	19	0.8	79355	2	AC021280	AC021280 Homo sapi
547	19	0.8	79494	2	AC068837	AC068837 Homo sapi
548	19	0.8	80817	9	AC146370	AC146370 Pan trogl
c 549	19	0.8	80828	5	AL672211	AL672211 Zebrafish
550	19	0.8	81149	2	AC023338	AC023338 Homo sapi
c 551	19	0.8	82980	9	AL954237	AL954237 Pan trogl
552	19	0.8	82998	2	AC022970	AC022970 Homo sapi
c 553	19	0.8	84348	5	BX649558	BX649558 Zebrafish
c 554	19	0.8	85297	9	AC079877	AC079877 Homo sapi
555	19	0.8	85565	3	AC084423	AC084423 Caenorhab
c 556	19	0.8	85782	2	AC134656	AC134656 Rattus no
557	19	0.8	88748	2	AC136733	AC136733 Mus muscu
c 558	19	0.8	88871	10	MMU58105	U58105 Mus musculu
559	19	0.8	92245	9	AC073968	AC073968 Homo sapi
560	19	0.8	92620	8	AB026636	AB026636 Arabidops
c 561	19	0.8	93287	9	AC023906	AC023906 Homo sapi
562	19	0.8	93942	2	AC136851	AC136851 Rattus no
563	19	0.8	94019	9	AL359971	AL359971 Human DNA
c 564	19	0.8	94255	9	AC003090	AC003090 Homo sapi
565	19	0.8	95185	8	ATF6I7	AL049657 Arabidops
c 566	19	0.8	97118	2	AC096323_4	Continuation (5 of
567	19	0.8	97473	9	AC127165	AC127165 Homo sapi
c 568	19	0.8	98119	2	AL357076	AL357076 Homo sapi
569	19	0.8	98391	9	AC106733	AC106733 Homo sapi
c 570	19	0.8	98415	2	AC093587	AC093587 Homo sapi
571	19	0.8	98461	8	ATT6H20	AL096859 Arabidops
c 572	19	0.8	99108	5	BX537146	BX537146 Zebrafish
c 573	19	0.8	99173	9	AL139800	AL139800 Human DNA

574	19	0.8	99340	9	HSDJ770C6	AL109932 Human DNA
c 575	19	0.8	99886	9	HS598F2	AL021579 Human DNA
576	19	0.8	100731	9	AC084030	AC084030 Homo sapi
577	19	0.8	100909	2	AC134874	AC134874 Homo sapi
578	19	0.8	101458	2	AP000680	AP000680 Homo sapi
c 579	19	0.8	101817	9	HS1216H12	AL008715 Human DNA
580	19	0.8	101892	2	AC151425	AC151425 Medicago
c 581	19	0.8	102910	9	AB041512	AB041512 Homo sapi
582	19	0.8	103135	10	AL954178	AL954178 Mouse DNA
583	19	0.8	103574	9	HSAC002115	AC002115 Human DNA
584	19	0.8	103577	9	AC009449	AC009449 Homo sapi
c 585	19	0.8	103933	10	AL805900	AL805900 Mouse DNA
586	19	0.8	104776	9	AC022424	AC022424 Homo sapi
587	19	0.8	105582	2	AC139065	AC139065 Homo sapi
c 588	19	0.8	105686	9	AC012072	AC012072 Homo sapi
589	19	0.8	105935	5	BX548055	BX548055 Zebrafish
c 590	19	0.8	106429	2	AC132536_5	Continuation (6 of
c 591	19	0.8	106784	9	AF188029	AF188029 Homo sapi
592	19	0.8	108271	9	AL445438	AL445438 Human DNA
c 593	19	0.8	108534	9	HS12409	AL021327 Human DNA
c 594	19	0.8	110000	1	AE016827_15	Continuation (16 o
c 595	19	0.8	110000	1	AE017354_27	Continuation (28 o
c 596	19	0.8	110000	1	BX908798_15	Continuation (16 o
c 597	19	0.8	110000	1	BX936398_24	Continuation (25 o
c 598	19	0.8	110000	1	CP000001_40	Continuation (41 o
c 599	19	0.8	110000	1	CP000013_4	Continuation (5 of
c 600	19	0.8	110000	1	CR628336_28	Continuation (29 o
601	19	0.8	110000	2	AC095360_0	AC095360 Rattus no
c 602	19	0.8	110000	2	AC096323_3	Continuation (4 of
603	19	0.8	110000	2	AC107170_0	AC107170 Rattus no
c 604	19	0.8	110000	2	AC108632_3	Continuation (4 of
c 605	19	0.8	110000	2	AC110502_3	Continuation (4 of
606	19	0.8	110000	2	AC110675_3	Continuation (4 of
c 607	19	0.8	110000	2	AC112029_4	Continuation (5 of
608	19	0.8	110000	2	AC126822_1	Continuation (2 of
609	19	0.8	110000	2	AC142955_3	Continuation (4 of
610	19	0.8	110000	2	AC151734_0	AC151734 Mus muscu
c 611	19	0.8	110000	2	AL390202_01	Continuation (2 of
c 612	19	0.8	110000	2	AL928982_2	Continuation (3 of
c 613	19	0.8	110000	2	AL928982_3	Continuation (4 of
614	19	0.8	110000	8	CR382131_26	Continuation (27 o
615	19	0.8	110000	8	CR382131_27	Continuation (28 o
616	19	0.8	110983	2	AC110549	AC110549 Mus muscu
c 617	19	0.8	111074	9	AC007569	AC007569 Homo sapi
c 618	19	0.8	111372	2	AL353145	AL353145 Homo sapi
c 619	19	0.8	111731	2	BX323063	BX323063 Homo sapi
620	19	0.8	112902	9	AC034211	AC034211 Homo sapi
621	19	0.8	112997	2	AC151705	AC151705 Gallus ga
622	19	0.8	113196	9	HSJ697K14	AL121829 Human DNA
623	19	0.8	113798	10	AL591892	AL591892 Mouse DNA
624	19	0.8	114411	9	AC112909	AC112909 Homo sapi
c 625	19	0.8	114434	9	AC093728	AC093728 Homo sapi
626	19	0.8	115916	9	AC115220	AC115220 Homo sapi
c 627	19	0.8	116969	9	AL450423	AL450423 Human DNA
628	19	0.8	117101	9	AC004061	AC004061 Homo sapi
c 629	19	0.8	119335	2	AC150947	AC150947 Bos tauru
630	19	0.8	120612	9	AC108518	AC108518 Homo sapi

c 631	19	0.8	121483	4	BX323833	BX323833 Pig DNA s
632	19	0.8	123556	9	HS507I15	Z98950 Human DNA s
c 633	19	0.8	123742	9	AC069431	AC069431 Homo sapi
634	19	0.8	123766	2	AC151000	AC151000 Medicago
635	19	0.8	125151	9	AC093821	AC093821 Homo sapi
c 636	19	0.8	125360	9	AC117406	AC117406 Homo sapi
c 637	19	0.8	125425	10	AC102845	AC102845 Mus muscu
c 638	19	0.8	125803	8	ATF22K18	AL035356 Arabidops
c 639	19	0.8	127061	2	AC118593	AC118593 Mus muscu
c 640	19	0.8	127431	9	AC027796	AC027796 Homo sapi
641	19	0.8	127488	2	AC022095	AC022095 Homo sapi
642	19	0.8	127576	5	AC144824	AC144824 Danio rer
643	19	0.8	127686	2	AL591683	AL591683 Homo sapi
644	19	0.8	127841	2	AC147714	AC147714 Medicago
c 645	19	0.8	128059	4	AY386694	AY386694 Oryctolag
c 646	19	0.8	128338	2	CR774177	CR774177 Danio rer
647	19	0.8	128861	5	BX294435	BX294435 Zebrafish
648	19	0.8	129231	9	AC092265	AC092265 Homo sapi
c 649	19	0.8	129461	2	CR677748	CR677748 Danio rer
c 650	19	0.8	129818	10	AC101831	AC101831 Mus muscu
651	19	0.8	129831	10	AC147268	AC147268 Mus muscu
652	19	0.8	130065	2	AC120329	AC120329 Rattus no
653	19	0.8	130129	2	AC108083	AC108083 Homo sapi
654	19	0.8	130494	2	AL139422	AL139422 Homo sapi
655	19	0.8	131390	2	AC083986	AC083986 Homo sapi
c 656	19	0.8	131691	9	AC096765	AC096765 Homo sapi
657	19	0.8	131769	9	AC104506	AC104506 Homo sapi
658	19	0.8	132080	9	AC069368	AC069368 Homo sapi
c 659	19	0.8	133221	9	HS333A15	AL031429 Human DNA
660	19	0.8	133242	8	AP003140	AP003140 Oryza sat
c 661	19	0.8	133519	10	AC140473	AC140473 Mus muscu
662	19	0.8	133968	5	BX511174	BX511174 Zebrafish
663	19	0.8	134597	2	CR391983	CR391983 Danio rer
664	19	0.8	134972	2	CR388177	CR388177 Danio rer
c 665	19	0.8	134972	2	CR388177	CR388177 Danio rer
c 666	19	0.8	135063	10	AC099644	AC099644 Mus muscu
667	19	0.8	135384	5	BX927227	BX927227 Zebrafish
668	19	0.8	135453	2	AC118736	AC118736 Mus muscu
c 669	19	0.8	135800	2	AF523316	AF523316 Canis fam
670	19	0.8	137562	2	AC151181	AC151181 Bos tauru
c 671	19	0.8	137705	10	AC140228	AC140228 Mus muscu
672	19	0.8	137722	2	CR352240	CR352240 Danio rer
c 673	19	0.8	137830	2	AC024346	AC024346 Homo sapi
674	19	0.8	137926	8	AP004867	AP004867 Oryza sat
675	19	0.8	138634	10	AC140917	AC140917 Mus muscu
c 676	19	0.8	139058	2	AC145763	AC145763 Canis fam
c 677	19	0.8	139228	4	AC127467	AC127467 Atelerix
c 678	19	0.8	140023	4	AC093453	AC093453 Canis fam
679	19	0.8	140856	9	AC002430	AC002430 Human BAC
680	19	0.8	141466	2	AC110673	AC110673 Canis fam
681	19	0.8	141548	2	AC109184	AC109184 Mus muscu
c 682	19	0.8	142010	8	AP003928	AP003928 Oryza sat
683	19	0.8	143283	10	AC141877	AC141877 Mus muscu
684	19	0.8	143503	5	BX677663	BX677663 Zebrafish
c 685	19	0.8	143682	9	AC108743	AC108743 Homo sapi
c 686	19	0.8	144301	9	AC010467	AC010467 Homo sapi
c 687	19	0.8	144382	10	AC147149	AC147149 Mus muscu

c 688	19	0.8	144658	9	AL138969	AL138969 Human DNA
c 689	19	0.8	144870	2	AC012135	AC012135 Homo sapi
690	19	0.8	145028	9	AC073875	AC073875 Homo sapi
691	19	0.8	145491	8	AP002883	AP002883 Oryza sat
692	19	0.8	145736	9	AL451139	AL451139 Human DNA
c 693	19	0.8	145962	2	CR352215	CR352215 Danio rer
694	19	0.8	145972	10	AC145608	AC145608 Mus muscu
695	19	0.8	145992	9	AC134919	AC134919 Homo sapi
696	19	0.8	146128	9	AC026358	AC026358 Homo sapi
697	19	0.8	146308	2	AC104751	AC104751 Mus muscu
698	19	0.8	146335	8	AP002521	AP002521 Oryza sat
699	19	0.8	146346	2	AC111120	AC111120 Mus muscu
c 700	19	0.8	146372	9	AL359174	AL359174 Human DNA
701	19	0.8	146383	2	AC016052	AC016052 Homo sapi
702	19	0.8	146410	9	AC006975	AC006975 Homo sapi
c 703	19	0.8	146442	10	AC099600	AC099600 Mus muscu
c 704	19	0.8	146885	2	BX957322	BX957322 Danio rer
c 705	19	0.8	147113	10	AC115033	AC115033 Mus muscu
706	19	0.8	147309	6	AX528392	AX528392 Sequence
707	19	0.8	148204	2	AC113238	AC113238 Felis cat
c 708	19	0.8	148656	9	AC005482	AC005482 Homo sapi
c 709	19	0.8	148737	9	AC026702	AC026702 Homo sapi
c 710	19	0.8	148801	9	AC100808	AC100808 Homo sapi
c 711	19	0.8	149298	2	AC119738	AC119738 Homo sapi
c 712	19	0.8	149320	2	AC126357	AC126357 Homo sapi
c 713	19	0.8	149579	10	AC147996	AC147996 Mus muscu
c 714	19	0.8	149712	2	AC140853	AC140853 Canis fam
c 715	19	0.8	150024	9	HS522P13	AL024509 Human DNA
c 716	19	0.8	150102	4	AY423389	AY423389 Canis fam
717	19	0.8	150150	8	AP002539	AP002539 Oryza sat
c 718	19	0.8	150186	10	AC140493	AC140493 Mus muscu
c 719	19	0.8	150573	9	AC097473	AC097473 Homo sapi
c 720	19	0.8	150641	5	AL935205	AL935205 Zebrafish
721	19	0.8	150751	9	AC092609	AC092609 Homo sapi
722	19	0.8	150772	2	AC131917	AC131917 Mus muscu
723	19	0.8	150957	8	OSJN00055	AL606628 Oryza sat
724	19	0.8	151152	6	CQ861610	CQ861610 Sequence
725	19	0.8	151152	9	HS454M7	AL022162 Human DNA
726	19	0.8	151163	9	HSA305P22	AL121673 Human DNA
727	19	0.8	151569	2	AC127473	AC127473 Canis fam
c 728	19	0.8	151628	2	AC016665	AC016665 Homo sapi
c 729	19	0.8	151655	9	AC012158	AC012158 Homo sapi
730	19	0.8	151874	2	AC011268	AC011268 Homo sapi
731	19	0.8	152341	9	AL137848	AL137848 Human DNA
732	19	0.8	152416	5	BX537336	BX537336 Zebrafish
733	19	0.8	152707	2	AC140215	AC140215 Mus muscu
c 734	19	0.8	152853	10	AC133082	AC133082 Mus muscu
735	19	0.8	152901	2	AC141346	AC141346 Rattus no
c 736	19	0.8	153001	10	AC147183	AC147183 Mus muscu
c 737	19	0.8	153021	10	AL663042	AL663042 Mouse DNA
738	19	0.8	153093	10	AC121939	AC121939 Mus muscu
c 739	19	0.8	153402	9	HS247E2	AL773569 Homo sapi
740	19	0.8	153746	9	AC108125	AC108125 Homo sapi
741	19	0.8	153866	2	AC137914	AC137914 Felis cat
c 742	19	0.8	153897	5	AL928656	AL928656 Zebrafish
743	19	0.8	154154	9	HS462023	AL031431 Human DNA
744	19	0.8	154280	10	AC147622	AC147622 Mus muscu

c 745	19	0.8	154495	2	AC016646	AC016646 Homo sapi
c 746	19	0.8	154540	8	AP004632	AP004632 Oryza sat
747	19	0.8	154648	10	AC145583	AC145583 Mus muscu
748	19	0.8	154818	9	AL157711	AL157711 Human DNA
749	19	0.8	154936	2	AC137907	AC137907 Canis fam
c 750	19	0.8	155179	10	AC132322	AC132322 Mus muscu
751	19	0.8	155369	9	AL160058	AL160058 Human DNA
c 752	19	0.8	155490	2	AC015478	AC015478 Homo sapi
753	19	0.8	155536	9	AC004112	AC004112 Homo sapi
c 754	19	0.8	155587	2	AC022053	AC022053 Homo sapi
c 755	19	0.8	155618	2	CR405702	CR405702 Danio rer
756	19	0.8	155848	9	AC104996	AC104996 Homo sapi
c 757	19	0.8	156048	10	AC145562	AC145562 Mus muscu
758	19	0.8	156577	10	AC140239	AC140239 Mus muscu
c 759	19	0.8	156656	9	AC021820	AC021820 Homo sapi
760	19	0.8	156821	9	AC005691	AC005691 Homo sapi
761	19	0.8	157042	2	CR759826	CR759826 Danio rer
762	19	0.8	157216	9	AC087491	AC087491 Homo sapi
763	19	0.8	157662	5	BX927072	BX927072 Zebrafish
764	19	0.8	157783	2	AC119202	AC119202 Mus muscu
765	19	0.8	157996	10	AC019026	AC019026 Mus muscu
766	19	0.8	158018	5	AL953896	AL953896 Zebrafish
767	19	0.8	158045	9	AC007432	AC007432 Homo sapi
c 768	19	0.8	158206	2	AC022661	AC022661 Homo sapi
c 769	19	0.8	158267	2	AC149770	AC149770 Bos tauru
770	19	0.8	158387	2	AC095020	AC095020 Bos tauru
771	19	0.8	158617	9	AC135972	AC135972 Homo sapi
772	19	0.8	158678	10	AC108822	AC108822 Mus muscu
773	19	0.8	158760	2	AC026098	AC026098 Homo sapi
774	19	0.8	158872	10	AC133178	AC133178 Mus muscu
c 775	19	0.8	159320	9	AP006197	AP006197 Homo sapi
776	19	0.8	159348	10	AC145373	AC145373 Mus muscu
c 777	19	0.8	159397	2	AC027040	AC027040 Homo sapi
778	19	0.8	159419	5	AC144823	AC144823 Danio rer
779	19	0.8	159605	2	AC120405	AC120405 Mus muscu
c 780	19	0.8	159927	9	AL353590	AL353590 Human DNA
781	19	0.8	160138	9	AC008551	AC008551 Homo sapi
782	19	0.8	160425	9	AL592153	AL592153 Human DNA
783	19	0.8	160629	10	BX248578	BX248578 Mouse DNA
784	19	0.8	160712	9	AC098799	AC098799 Homo sapi
785	19	0.8	160781	2	AC128871	AC128871 Rattus no
786	19	0.8	160796	10	AL592222	AL592222 Mouse DNA
787	19	0.8	160891	9	AL512410	AL512410 Human DNA
c 788	19	0.8	161048	9	AC144510	AC144510 Pan trogl
789	19	0.8	161070	2	AC149700	AC149700 Bos tauru
790	19	0.8	161222	2	AC016037	AC016037 Homo sapi
791	19	0.8	161640	2	AC119229	AC119229 Mus muscu
c 792	19	0.8	161647	9	AC079080	AC079080 Homo sapi
c 793	19	0.8	161830	9	AC110619	AC110619 Homo sapi
794	19	0.8	162126	2	AC011784	AC011784 Homo sapi
c 795	19	0.8	162126	9	AL354711	AL354711 Human DNA
c 796	19	0.8	162132	10	AC147142	AC147142 Mus muscu
c 797	19	0.8	162345	2	AC147606	AC147606 Mus muscu
798	19	0.8	162407	8	AP004121	AP004121 Oryza sat
c 799	19	0.8	162538	2	BX649414	BX649414 Homo sapi
800	19	0.8	162743	10	AC144581	AC144581 Mus muscu
c 801	19	0.8	162932	2	AC018516	AC018516 Homo sapi

c 802	19	0.8	162935	10	AL359352	AL359352 Mouse DNA
803	19	0.8	162981	10	AL844204	AL844204 Mouse DNA
c 804	19	0.8	162993	9	AC108105	AC108105 Homo sapi
c 805	19	0.8	163018	10	AC132254	AC132254 Mus muscu
c 806	19	0.8	163061	2	AC141982	AC141982 Rattus no
807	19	0.8	163149	9	CNS01DSZ	AL122057 Human chr
c 808	19	0.8	163183	3	AC009842	AC009842 Drosophil
c 809	19	0.8	163377	2	AC007897	AC007897 Homo sapi
810	19	0.8	163419	5	BX323847	BX323847 Zebrafish
811	19	0.8	163796	9	AC093725	AC093725 Homo sapi
c 812	19	0.8	163892	10	AC134567	AC134567 Mus muscu
813	19	0.8	164612	10	AC124697	AC124697 Mus muscu
c 814	19	0.8	164702	6	AX706960	AX706960 Sequence
c 815	19	0.8	164702	6	AX707890	AX707890 Sequence
c 816	19	0.8	165151	2	BX936362	BX936362 Danio rer
c 817	19	0.8	165290	10	AC136638	AC136638 Mus muscu
c 818	19	0.8	165500	9	AP005139	AP005139 Homo sapi
c 819	19	0.8	165651	2	AC151393	AC151393 Atelerix
820	19	0.8	165699	2	AP001802	AP001802 Homo sapi
821	19	0.8	165777	10	BX004852	BX004852 Mouse DNA
c 822	19	0.8	165828	10	AC132283	AC132283 Mus muscu
c 823	19	0.8	165926	10	AC119876	AC119876 Mus muscu
c 824	19	0.8	165990	2	AC073509	AC073509 Homo sapi
c 825	19	0.8	166107	2	AC134334	AC134334 Mus muscu
826	19	0.8	166138	9	AC099684	AC099684 Homo sapi
c 827	19	0.8	166183	9	AC073048	AC073048 Homo sapi
c 828	19	0.8	166257	9	AC012083	AC012083 Homo sapi
c 829	19	0.8	166306	9	AC022880	AC022880 Homo sapi
c 830	19	0.8	166451	2	AC025511	AC025511 Homo sapi
831	19	0.8	166626	3	AC008318	AC008318 Drosophil
c 832	19	0.8	166651	4	AC087160	AC087160 Sus scrof
833	19	0.8	166768	10	AC122796	AC122796 Mus muscu
834	19	0.8	166777	2	AC106813	AC106813 Homo sapi
c 835	19	0.8	167022	9	AC010238	AC010238 Homo sapi
836	19	0.8	167058	10	AL596183	AL596183 Mouse DNA
837	19	0.8	167075	2	AC137909	AC137909 Canis fam
838	19	0.8	167334	2	AC026034	AC026034 Homo sapi
839	19	0.8	167734	9	AL157827	AL157827 Human DNA
c 840	19	0.8	167780	9	AL844892	AL844892 Human DNA
841	19	0.8	167796	5	BX571826	BX571826 Zebrafish
842	19	0.8	167878	9	AC096645	AC096645 Homo sapi
c 843	19	0.8	167940	2	CR356231	CR356231 Danio rer
c 844	19	0.8	168347	2	AC025336	AC025336 Homo sapi
845	19	0.8	168569	10	AL671970	AL671970 Mouse DNA
846	19	0.8	168601	10	AC132276	AC132276 Mus muscu
c 847	19	0.8	168608	2	AC090464	AC090464 Homo sapi
848	19	0.8	168623	9	AC007649	AC007649 Homo sapi
849	19	0.8	168624	9	AC092131	AC092131 Homo sapi
c 850	19	0.8	168668	10	AC138289	AC138289 Mus muscu
851	19	0.8	168940	2	AC102307	AC102307 Mus muscu
852	19	0.8	169046	5	AL928828	AL928828 Zebrafish
c 853	19	0.8	169393	9	AC146016	AC146016 Pan trogl
854	19	0.8	169539	2	AC080095	AC080095 Homo sapi
855	19	0.8	169628	5	BX322567	BX322567 Zebrafish
c 856	19	0.8	169686	2	BX465864	BX465864 Danio rer
857	19	0.8	169892	2	CR589945	CR589945 Danio rer
c 858	19	0.8	170017	2	AC148158	AC148158 Zea mays

c 859	19	0.8	170027	2	AC110670	AC110670	Canis fam
c 860	19	0.8	170139	2	CR388179	CR388179	Danio rer
c 861	19	0.8	170425	2	AC024490	AC024490	Homo sapi
c 862	19	0.8	170455	2	AC025054	AC025054	Homo sapi
c 863	19	0.8	170479	10	AC147985	AC147985	Mus muscu
864	19	0.8	170796	2	AC069416	AC069416	Homo sapi
865	19	0.8	170842	9	AC007384	AC007384	Homo sapi
866	19	0.8	170914	3	AC010843	AC010843	Drosophil
c 867	19	0.8	170914	3	AC010843	AC010843	Drosophil
868	19	0.8	170988	10	AC121950	AC121950	Mus muscu
869	19	0.8	171033	2	CR352213	CR352213	Danio rer
870	19	0.8	171185	2	AP002424	AP002424	Homo sapi
871	19	0.8	171188	2	AC005025	AC005025	Homo sapi
c 872	19	0.8	171266	2	BX323586	BX323586	Danio rer
c 873	19	0.8	171646	10	AC144851	AC144851	Mus muscu
c 874	19	0.8	171747	2	AC087678	AC087678	Homo sapi
c 875	19	0.8	171829	2	CR405711	CR405711	Danio rer
876	19	0.8	171912	10	AC147150	AC147150	Mus muscu
877	19	0.8	171982	2	AC120916	AC120916	Rattus no
878	19	0.8	172134	2	AC138589	AC138589	Mus muscu
c 879	19	0.8	172246	9	AC024941	AC024941	Homo sapi
c 880	19	0.8	172327	2	AC012345	AC012345	Homo sapi
c 881	19	0.8	172371	2	AC092871	AC092871	Pan trogl
882	19	0.8	172735	2	AC141005	AC141005	Rattus no
883	19	0.8	172845	9	AL160053	AL160053	Human DNA
884	19	0.8	172915	2	AC010160	AC010160	Homo sapi
885	19	0.8	173003	10	AC125155	AC125155	Mus muscu
886	19	0.8	173189	9	AC092323	AC092323	Homo sapi
c 887	19	0.8	173699	8	AP003416	AP003416	Oryza sat
c 888	19	0.8	173840	2	AC149585	AC149585	Mus muscu
889	19	0.8	173882	9	HSAF001550	AF001550	Homo sapi
c 890	19	0.8	174021	9	AL358612	AL358612	Human DNA
c 891	19	0.8	174032	2	AC025904	AC025904	Homo sapi
892	19	0.8	174033	2	AC021957	AC021957	Homo sapi
c 893	19	0.8	174116	2	AC026138	AC026138	Homo sapi
c 894	19	0.8	174152	10	AC132133	AC132133	Mus muscu
895	19	0.8	174218	2	AC091071	AC091071	Oryza sat
896	19	0.8	174269	2	AC132961	AC132961	Rattus no
c 897	19	0.8	174311	9	AP002788	AP002788	Homo sapi
898	19	0.8	174591	2	AC140582	AC140582	Macaca mu
c 899	19	0.8	174617	2	AC023671	AC023671	Homo sapi
c 900	19	0.8	174633	2	AC126418	AC126418	Mus muscu
901	19	0.8	174850	9	AL353745	AL353745	Human DNA
902	19	0.8	174882	9	AC010585	AC010585	Homo sapi
903	19	0.8	175294	10	AC145558	AC145558	Mus muscu
c 904	19	0.8	175317	9	AC104298	AC104298	Homo sapi
c 905	19	0.8	175406	10	AC131778	AC131778	Mus muscu
c 906	19	0.8	175421	2	AC140714	AC140714	Homo sapi
907	19	0.8	175672	2	AC068691	AC068691	Homo sapi
c 908	19	0.8	175727	2	AC120798	AC120798	Mus muscu
909	19	0.8	175747	2	BX571952	BX571952	Danio rer
c 910	19	0.8	175820	9	AL162378	AL162378	Human DNA
911	19	0.8	175822	2	AC068402	AC068402	Homo sapi
c 912	19	0.8	175840	9	AC019306	AC019306	Homo sapi
c 913	19	0.8	175934	2	AC123868	AC123868	Mus muscu
c 914	19	0.8	176117	9	AC092352	AC092352	Homo sapi
915	19	0.8	176153	9	AC006287	AC006287	Homo sapi

916	19	0.8	176249	2	BX950226	BX950226	Danio rer
917	19	0.8	176290	2	CR352241	CR352241	Homo sapi
c 918	19	0.8	176435	2	AC149874	AC149874	Xenopus t
c 919	19	0.8	176699	2	AC122967	AC122967	Rattus no
920	19	0.8	176952	2	AC113805	AC113805	Rattus no
c 921	19	0.8	176965	2	AC148164	AC148164	Zea mays
c 922	19	0.8	177097	2	AP001569	AP001569	Homo sapi
923	19	0.8	177223	10	AL663106	AL663106	Mouse DNA
c 924	19	0.8	177251	10	AC124565	AC124565	Mus muscu
c 925	19	0.8	177267	9	AC026116	AC026116	Homo sapi
c 926	19	0.8	177463	9	AP002853	AP002853	Homo sapi
927	19	0.8	177852	2	AC034283	AC034283	Homo sapi
c 928	19	0.8	177969	10	AC122306	AC122306	Mus muscu
c 929	19	0.8	178004	2	AL590070	AL590070	Homo sapi
930	19	0.8	178015	2	AC094993	AC094993	Rattus no
931	19	0.8	178030	9	AC008406	AC008406	Homo sapi
c 932	19	0.8	178501	2	AC146738	AC146738	Otolemur
c 933	19	0.8	178528	10	AC131662	AC131662	Mus muscu
c 934	19	0.8	178560	2	AC134877	AC134877	Homo sapi
935	19	0.8	178580	2	AC127948	AC127948	Rattus no
c 936	19	0.8	178780	9	AC121493	AC121493	Homo sapi
c 937	19	0.8	178981	2	AC149839	AC149839	Callithri
c 938	19	0.8	179110	9	AC011755	AC011755	Homo sapi
939	19	0.8	179328	2	AC142429	AC142429	Rattus no
940	19	0.8	179357	2	AC009625	AC009625	Homo sapi
c 941	19	0.8	179437	5	AL928892	AL928892	Zebrafish
c 942	19	0.8	179539	2	AC016369	AC016369	Homo sapi
c 943	19	0.8	179655	2	AC018940	AC018940	Homo sapi
c 944	19	0.8	179721	9	AC084356	AC084356	Homo sapi
945	19	0.8	179726	9	AC007052	AC007052	Homo sapi
c 946	19	0.8	179755	9	AL603831	AL603831	Human DNA
947	19	0.8	179840	2	AC068458	AC068458	Homo sapi
c 948	19	0.8	179941	10	AC142271	AC142271	Mus muscu
949	19	0.8	180049	9	AC099558	AC099558	Homo sapi
950	19	0.8	180520	2	AL714008	AL714008	Homo sapi
c 951	19	0.8	180530	10	AC136903	AC136903	Mus muscu
c 952	19	0.8	180563	2	AC034170	AC034170	Homo sapi
953	19	0.8	180586	2	AC108912	AC108912	Mus muscu
c 954	19	0.8	180675	10	AC147991	AC147991	Mus muscu
c 955	19	0.8	180733	5	BX530027	BX530027	Zebrafish
956	19	0.8	181034	2	AC135486	AC135486	Rattus no
c 957	19	0.8	181371	2	AC018893	AC018893	Homo sapi
c 958	19	0.8	181433	9	CNS00006	AL049775	Human chr
959	19	0.8	181660	2	CR382295	CR382295	Danio rer
960	19	0.8	181755	10	AC129289	AC129289	Mus muscu
c 961	19	0.8	181957	9	AC146382	AC146382	Pan trogl
c 962	19	0.8	182135	10	AC124184	AC124184	Mus muscu
c 963	19	0.8	182173	2	AC140974	AC140974	Papio ham
964	19	0.8	182248	10	AL606915	AL606915	Mouse DNA
c 965	19	0.8	182256	9	AC005058	AC005058	Homo sapi
966	19	0.8	182411	2	AC090408	AC090408	Homo sapi
967	19	0.8	182534	10	AC101948	AC101948	Mus muscu
c 968	19	0.8	182586	2	AC053505	AC053505	Homo sapi
c 969	19	0.8	182741	2	AC112855	AC112855	Rattus no
c 970	19	0.8	182774	5	BX284646	BX284646	Zebrafish
971	19	0.8	182798	2	AC025394	AC025394	Homo sapi
972	19	0.8	182857	2	AC147219	AC147219	Mus muscu

c 973	19	0.8	182960	9	CNS01RHW	AL162551	Human chr
974	19	0.8	183093	9	AC138688	AC138688	Homo sapi
975	19	0.8	183121	2	AC093417	AC093417	Homo sapi
c 976	19	0.8	183133	10	AC101851	AC101851	Mus muscu
c 977	19	0.8	183315	10	AC140383	AC140383	Mus muscu
c 978	19	0.8	183707	10	AC124384	AC124384	Mus muscu
979	19	0.8	183894	9	AC040970	AC040970	Homo sapi
980	19	0.8	183901	2	AL356425	AL356425	Homo sapi
c 981	19	0.8	183987	10	AC145344	AC145344	Mus muscu
c 982	19	0.8	184490	2	AC123734	AC123734	Mus muscu
983	19	0.8	184663	2	AC012113	AC012113	Homo sapi
984	19	0.8	184769	9	AC016583	AC016583	Homo sapi
985	19	0.8	184822	2	AC118743	AC118743	Mus muscu
c 986	19	0.8	184966	2	AC146675	AC146675	Callithri
c 987	19	0.8	185095	8	AP003436	AP003436	Oryza sat
c 988	19	0.8	185174	9	AC073091	AC073091	Homo sapi
c 989	19	0.8	185417	9	AC012313	AC012313	Homo sapi
990	19	0.8	185481	2	AC091088	AC091088	Oryza sat
991	19	0.8	185573	2	AC010994	AC010994	Drosophil
c 992	19	0.8	185621	2	AC036195	AC036195	Homo sapi
c 993	19	0.8	185945	2	CR293528	CR293528	Danio rer
c 994	19	0.8	186078	9	AC037482	AC037482	Homo sapi
c 995	19	0.8	186278	9	AL928717	AL928717	Human DNA
996	19	0.8	186673	2	AL590713	AL590713	Homo sapi
997	19	0.8	187023	2	AC006882	AC006882	Caenorhab
998	19	0.8	187032	10	AC147372	AC147372	Mus muscu
c 999	19	0.8	187084	9	AC010269	AC010269	Homo sapi
c1000	19	0.8	187316	9	AL139340	AL139340	Human DNA
c1001	19	0.8	187367	2	AC099751	AC099751	Sus scrof
c1002	19	0.8	187490	2	AL691495	AL691495	Homo sapi
1003	19	0.8	187691	5	BX324194	BX324194	Zebrafish
1004	19	0.8	187738	10	AL845547	AL845547	Mouse DNA
c1005	19	0.8	187948	2	BX005227	BX005227	Danio rer
c1006	19	0.8	187960	9	AP000866	AP000866	Homo sapi
c1007	19	0.8	188285	9	AL135842	AL135842	Human DNA
c1008	19	0.8	188322	2	AC134541	AC134541	Mus muscu
1009	19	0.8	188330	2	AC139710	AC139710	Canis fam
1010	19	0.8	188333	9	AC146143	AC146143	Pan trogl
1011	19	0.8	188435	10	AC100263	AC100263	Mus muscu
c1012	19	0.8	188548	9	AC008661	AC008661	Homo sapi
c1013	19	0.8	188724	10	AC142113	AC142113	Mus muscu
1014	19	0.8	188844	2	AC127475	AC127475	Canis fam
1015	19	0.8	188895	5	BX004834	BX004834	Zebrafish
1016	19	0.8	188945	2	AC093697	AC093697	Homo sapi
1017	19	0.8	188951	2	AC126762	AC126762	Homo sapi
1018	19	0.8	189160	2	AC080074	AC080074	Homo sapi
1019	19	0.8	189272	2	AC119503	AC119503	Rattus no
c1020	19	0.8	189371	2	AC090230	AC090230	Homo sapi
1021	19	0.8	189490	10	AC136975	AC136975	Mus muscu
1022	19	0.8	189507	10	AC132441	AC132441	Mus muscu
1023	19	0.8	189728	10	AC140223	AC140223	Mus muscu
1024	19	0.8	189770	9	AC147329	AC147329	Pan trogl
1025	19	0.8	189814	9	AC145866	AC145866	Pan trogl
c1026	19	0.8	189822	9	AC092722	AC092722	Homo sapi
c1027	19	0.8	189828	2	AC069321	AC069321	Homo sapi
c1028	19	0.8	189903	2	AC012542	AC012542	Homo sapi
c1029	19	0.8	190024	9	AC122714	AC122714	Homo sapi

1030	19	0.8	190437	10	AC098724	AC098724 Mus muscu
c1031	19	0.8	190627	10	AL671982	AL671982 Mouse DNA
c1032	19	0.8	190648	9	CNS01DXI	AL139317 Human chr
1033	19	0.8	190649	2	BX663608	BX663608 Danio rer
1034	19	0.8	191121	2	AC083952	AC083952 Homo sapi
c1035	19	0.8	191191	9	AC000119	AC000119 Homo sapi
1036	19	0.8	191218	8	OSJN00171	AL662974 Oryza sat
c1037	19	0.8	191453	5	BX510648	BX510648 Zebrafish
c1038	19	0.8	191602	2	AC068920	AC068920 Homo sapi
1039	19	0.8	191613	10	AC132408	AC132408 Mus muscu
c1040	19	0.8	191665	9	AC027627	AC027627 Homo sapi
c1041	19	0.8	191856	9	AL355980	AL355980 Human DNA
1042	19	0.8	191942	9	AC079951	AC079951 Homo sapi
1043	19	0.8	192016	10	AC099582	AC099582 Mus muscu
c1044	19	0.8	192273	2	AC137982	AC137982 Mus muscu
c1045	19	0.8	192338	2	AC022221	AC022221 Homo sapi
1046	19	0.8	192584	10	AC131080	AC131080 Mus muscu
1047	19	0.8	192658	2	AC132225	AC132225 Mus muscu
1048	19	0.8	193001	2	AC151369	AC151369 Aotus nan
1049	19	0.8	193064	2	AC124333	AC124333 Mus muscu
1050	19	0.8	193153	2	AC141895	AC141895 Mus muscu
1051	19	0.8	193167	2	AC117938	AC117938 Canis fam
c1052	19	0.8	193279	9	AC009466	AC009466 Homo sapi
c1053	19	0.8	193526	3	AC010993	AC010993 Drosophil
c1054	19	0.8	193549	9	AC087286	AC087286 Homo sapi
1055	19	0.8	193811	10	AC134827	AC134827 Mus muscu
c1056	19	0.8	193944	4	AC147679	AC147679 Canis Fam
1057	19	0.8	193963	9	AC007336	AC007336 Homo sapi
1058	19	0.8	194048	2	AC147652	AC147652 Pan trogl
c1059	19	0.8	194065	10	AL772179	AL772179 Mouse DNA
c1060	19	0.8	194109	10	AC121819	AC121819 Mus muscu
c1061	19	0.8	194224	5	BX465842	BX465842 Zebrafish
1062	19	0.8	194301	2	AC103772	AC103772 Homo sapi
1063	19	0.8	194335	10	AC144934	AC144934 Mus muscu
c1064	19	0.8	194615	2	AC024190	AC024190 Homo sapi
1065	19	0.8	194631	2	BX936384	BX936384 Danio rer
1066	19	0.8	194845	2	AC123885	AC123885 Mus muscu
c1067	19	0.8	194994	2	AC020609	AC020609 Homo sapi
c1068	19	0.8	195156	2	AC019034	AC019034 Homo sapi
c1069	19	0.8	195333	2	AC134255	AC134255 Mus muscu
1070	19	0.8	195413	10	AL671881	AL671881 Mouse DNA
1071	19	0.8	195444	2	AC025424	AC025424 Mus muscu
1072	19	0.8	195480	2	CR847999	CR847999 Danio rer
c1073	19	0.8	195488	2	CR753885	CR753885 Danio rer
1074	19	0.8	195858	2	AC023879	AC023879 Homo sapi
c1075	19	0.8	195950	9	AC012003	AC012003 Homo sapi
1076	19	0.8	195981	2	AC112959	AC112959 Mus muscu
1077	19	0.8	195992	10	AC103618	AC103618 Mus muscu
1078	19	0.8	196099	10	AC147113	AC147113 Mus muscu
1079	19	0.8	196361	2	AC123351	AC123351 Rattus no
c1080	19	0.8	196372	10	AL929100	AL929100 Mouse DNA
1081	19	0.8	196501	9	AC005908	AC005908 Homo sapi
c1082	19	0.8	196712	10	AC137902	AC137902 Mus muscu
1083	19	0.8	196734	2	AC010640	AC010640 Homo sapi
c1084	19	0.8	196869	2	AC087535	AC087535 Homo sapi
1085	19	0.8	197070	8	ATCHRIV62	AL161562 Arabidops
1086	19	0.8	197164	9	AC064865	AC064865 Homo sapi

c1087	19	0.8	197281	2	CR762408	CR762408	Danio rer
1088	19	0.8	197330	2	AL928858	AL928858	Danio rer
1089	19	0.8	197519	2	AC145553	AC145553	Mus muscu
c1090	19	0.8	197582	2	AC151934	AC151934	Callithri
1091	19	0.8	197602	10	AC147252	AC147252	Mus muscu
1092	19	0.8	197605	2	AC026905	AC026905	Homo sapi
1093	19	0.8	197630	9	AC011676	AC011676	Homo sapi
1094	19	0.8	197652	9	AC012074	AC012074	Homo sapi
c1095	19	0.8	197946	10	AC098722	AC098722	Mus muscu
1096	19	0.8	197949	10	AC122204	AC122204	Mus muscu
c1097	19	0.8	197978	10	AC114821	AC114821	Mus muscu
c1098	19	0.8	198237	2	AC026299	AC026299	Homo sapi
1099	19	0.8	198242	10	AC116489	AC116489	Mus muscu
1100	19	0.8	198244	2	CR381546	CR381546	Danio rer
1101	19	0.8	198470	9	AC046170	AC046170	Homo sapi
c1102	19	0.8	198644	9	AL590964	AL590964	Human DNA
1103	19	0.8	198935	9	AC034268	AC034268	Homo sapi
c1104	19	0.8	198942	9	AC008517	AC008517	Homo sapi
c1105	19	0.8	198991	2	AC102227	AC102227	Mus muscu
c1106	19	0.8	199024	2	AC150721	AC150721	Callithri
1107	19	0.8	199702	2	AC087178	AC087178	Homo sapi
1108	19	0.8	199733	10	AC144647	AC144647	Mus muscu
c1109	19	0.8	199848	10	AL512647	AL512647	Mouse DNA
1110	19	0.8	199883	2	AC073736	AC073736	Mus muscu
c1111	19	0.8	199916	3	AC008099	AC008099	Drosophil
1112	19	0.8	200237	9	AF168787	AF168787	Homo sapi
c1113	19	0.8	200278	9	AC092797	AC092797	Homo sapi
1114	19	0.8	200420	9	AC138645	AC138645	Homo sapi
c1115	19	0.8	200774	2	AP001592	AP001592	Homo sapi
1116	19	0.8	200840	9	AL158072	AL158072	Human DNA
c1117	19	0.8	201139	10	AC122865	AC122865	Mus muscu
1118	19	0.8	201279	9	AC090133	AC090133	Homo sapi
1119	19	0.8	201376	2	AC112449	AC112449	Rattus no
c1120	19	0.8	201418	2	AC144493	AC144493	Bos tauru
c1121	19	0.8	201611	2	AC021185	AC021185	Homo sapi
c1122	19	0.8	201757	10	AC061963	AC061963	Mus muscu
1123	19	0.8	201917	2	AC108015	AC108015	Homo sapi
c1124	19	0.8	201964	10	MMHHC29N7	AF030001	Mus muscu
c1125	19	0.8	201986	10	AC006289	AC006289	Mus muscu
1126	19	0.8	202083	2	AC023833	AC023833	Mus muscu
1127	19	0.8	202338	10	AC147107	AC147107	Mus muscu
1128	19	0.8	202442	2	AC110203	AC110203	Mus muscu
1129	19	0.8	202600	2	AC151374	AC151374	Callithri
1130	19	0.8	202609	2	AC102911	AC102911	Mus muscu
1131	19	0.8	202772	2	CR384110	CR384110	Danio rer
1132	19	0.8	202955	9	AL356378	AL356378	Human DNA
c1133	19	0.8	203169	2	BX571855	BX571855	Danio rer
1134	19	0.8	203412	2	AC107270	AC107270	Rattus no
c1135	19	0.8	203427	2	AC111331	AC111331	Rattus no
1136	19	0.8	203486	10	AC131733	AC131733	Mus muscu
1137	19	0.8	203718	9	AC009486	AC009486	Homo sapi
c1138	19	0.8	203810	10	AC132612	AC132612	Mus muscu
1139	19	0.8	203838	2	AC026840	AC026840	Homo sapi
1140	19	0.8	203944	10	AC145292	AC145292	Mus muscu
c1141	19	0.8	204044	2	AC146926	AC146926	Callithri
c1142	19	0.8	204198	2	BX470261	BX470261	Danio rer
c1143	19	0.8	204724	10	AC131912	AC131912	Mus muscu

c1144	19	0.8	204944	2	BX537255	BX537255	Danio rer
c1145	19	0.8	204950	10	AC083817	AC083817	Mus muscu
1146	19	0.8	205004	9	AC090132	AC090132	Homo sapi
1147	19	0.8	205029	2	AC118189	AC118189	Rattus no
1148	19	0.8	205044	2	AC024453	AC024453	Homo sapi
c1149	19	0.8	205222	10	AC123534	AC123534	Mus muscu
c1150	19	0.8	205572	2	AC055724	AC055724	Homo sapi
1151	19	0.8	205816	10	AC113201	AC113201	Mus muscu
c1152	19	0.8	205859	2	AC099702	AC099702	Mus muscu
c1153	19	0.8	205903	9	AP000901	AP000901	Homo sapi
c1154	19	0.8	205993	2	AC119212	AC119212	Mus muscu
1155	19	0.8	206021	9	AC012065	AC012065	Homo sapi
c1156	19	0.8	206023	2	AC146657	AC146657	Otolemur
c1157	19	0.8	206187	2	AC069139	AC069139	Homo sapi
c1158	19	0.8	206494	10	AC138766	AC138766	Mus muscu
c1159	19	0.8	206537	9	AC099777	AC099777	Homo sapi
1160	19	0.8	206618	9	AF195953	AF195953	Homo sapi
c1161	19	0.8	206630	2	AC150604	AC150604	Callithri
c1162	19	0.8	206783	10	AC139297	AC139297	Mus muscu
c1163	19	0.8	206817	2	AC128877	AC128877	Rattus no
c1164	19	0.8	206924	10	AC087780	AC087780	Mus muscu
c1165	19	0.8	207058	5	BX004794	BX004794	Zebrafish
1166	19	0.8	207199	2	CR376853	CR376853	Danio rer
c1167	19	0.8	207743	4	AC121066	AC121066	Oryctolag
c1168	19	0.8	207957	2	AC113746	AC113746	Rattus no
c1169	19	0.8	208229	2	CR388416	CR388416	Danio rer
1170	19	0.8	208296	2	AC099124	AC099124	Rattus no
c1171	19	0.8	208333	2	AC112848	AC112848	Rattus no
1172	19	0.8	208445	2	AC136119	AC136119	Rattus no
c1173	19	0.8	208678	10	AC116575	AC116575	Mus muscu
c1174	19	0.8	208685	2	AC145726	AC145726	Zea mays
1175	19	0.8	208963	2	BX936390	BX936390	Danio rer
1176	19	0.8	209083	10	AC113999	AC113999	Mus muscu
c1177	19	0.8	209112	9	AC010252	AC010252	Homo sapi
1178	19	0.8	209153	2	BX324130	BX324130	Danio rer
1179	19	0.8	209157	2	AC110856	AC110856	Rattus no
c1180	19	0.8	209258	2	AC151027	AC151027	Callithri
1181	19	0.8	209416	2	AC149219	AC149219	Mus muscu
c1182	19	0.8	209866	2	BX546466	BX546466	Danio rer
1183	19	0.8	209927	2	AC150904	AC150904	Pan trogl
c1184	19	0.8	210201	2	CR847962	CR847962	Danio rer
c1185	19	0.8	210320	9	AC093873	AC093873	Homo sapi
1186	19	0.8	210532	9	AC008558	AC008558	Homo sapi
c1187	19	0.8	210793	2	AC109120	AC109120	Rattus no
1188	19	0.8	211251	2	AC121029	AC121029	Rattus no
c1189	19	0.8	211349	10	AL627102	AL627102	Mouse DNA
c1190	19	0.8	211657	10	AL732564	AL732564	Mouse DNA
1191	19	0.8	211910	10	AC116573	AC116573	Mus muscu
c1192	19	0.8	211926	10	AC111092	AC111092	Mus muscu
c1193	19	0.8	212314	5	BX248090	BX248090	Zebrafish
1194	19	0.8	213015	2	AC118195	AC118195	Mus muscu
1195	19	0.8	213439	2	AC149849	AC149849	Papio anu
c1196	19	0.8	213684	10	AC132616	AC132616	Mus muscu
1197	19	0.8	214061	10	AL732571	AL732571	Mouse DNA
c1198	19	0.8	214071	10	AC113102	AC113102	Mus muscu
c1199	19	0.8	214399	10	AC147156	AC147156	Mus muscu
1200	19	0.8	214610	2	BX323578	BX323578	Danio rer

c1201	19	0.8	214610	2	BX323578	BX323578	Danio rer
c1202	19	0.8	215251	10	AC124183	AC124183	Mus muscu
1203	19	0.8	215499	2	BX511257	BX511257	Danio rer
1204	19	0.8	216069	2	AC122086	AC122086	Rattus no
c1205	19	0.8	216878	10	AC147109	AC147109	Mus muscu
c1206	19	0.8	216958	2	AC126465	AC126465	Rattus no
c1207	19	0.8	217278	10	AL604024	AL604024	Mouse DNA
c1208	19	0.8	217384	2	AC023573	AC023573	Homo sapi
1209	19	0.8	217829	10	AL840637	AL840637	Mouse DNA
c1210	19	0.8	218157	2	AC134263	AC134263	Rattus no
c1211	19	0.8	218226	2	AC126634	AC126634	Rattus no
1212	19	0.8	218427	10	AL645727	AL645727	Mouse DNA
1213	19	0.8	218442	2	AC135652	AC135652	Rattus no
1214	19	0.8	218988	2	AC129861	AC129861	Rattus no
c1215	19	0.8	219129	2	AC142415	AC142415	Mus muscu
1216	19	0.8	219341	2	AC114172	AC114172	Rattus no
c1217	19	0.8	219344	2	AC087864	AC087864	Homo sapi
c1218	19	0.8	219616	2	AC112398	AC112398	Rattus no
1219	19	0.8	220612	2	AC112466	AC112466	Rattus no
1220	19	0.8	220788	2	AC130904	AC130904	Rattus no
c1221	19	0.8	221004	9	CNS01DRW	AL121576	Human chr
1222	19	0.8	221128	10	AC123846	AC123846	Mus muscu
c1223	19	0.8	221356	2	AC130588	AC130588	Rattus no
c1224	19	0.8	221801	2	AC128780	AC128780	Rattus no
c1225	19	0.8	221972	2	CR388218	CR388218	Danio rer
c1226	19	0.8	222571	2	AC110338	AC110338	Rattus no
c1227	19	0.8	222814	10	AC134591	AC134591	Mus muscu
1228	19	0.8	223295	2	BX649623	BX649623	Homo sapi
1229	19	0.8	223513	2	AC111919	AC111919	Rattus no
c1230	19	0.8	223630	2	AC130986	AC130986	Rattus no
1231	19	0.8	223730	2	AC140553	AC140553	Mus muscu
c1232	19	0.8	223744	2	CR450774	CR450774	Danio rer
c1233	19	0.8	223890	2	AC062008	AC062008	Homo sapi
1234	19	0.8	223979	2	AC096151	AC096151	Rattus no
1235	19	0.8	224100	2	AC119827	AC119827	Mus muscu
c1236	19	0.8	224451	2	AC132772	AC132772	Rattus no
c1237	19	0.8	224514	2	CR376802	CR376802	Danio rer
c1238	19	0.8	224552	2	AC134092	AC134092	Rattus no
c1239	19	0.8	225035	10	AC145598	AC145598	Mus muscu
c1240	19	0.8	225089	2	AC126666	AC126666	Rattus no
1241	19	0.8	225187	2	AC094836	AC094836	Rattus no
1242	19	0.8	225300	2	AC084798	AC084798	Mus muscu
c1243	19	0.8	225846	2	AC109040	AC109040	Rattus no
1244	19	0.8	225865	2	AC118678	AC118678	Mus muscu
c1245	19	0.8	225893	2	AC103259	AC103259	Rattus no
c1246	19	0.8	226027	2	AC107580	AC107580	Rattus no
c1247	19	0.8	226581	2	AC128234	AC128234	Rattus no
c1248	19	0.8	226589	2	AC117299	AC117299	Rattus no
1249	19	0.8	226631	2	AC025501	AC025501	Mus muscu
c1250	19	0.8	226696	9	AC139026	AC139026	Homo sapi
1251	19	0.8	226740	2	AC112661	AC112661	Mus muscu
c1252	19	0.8	226740	2	AC112661	AC112661	Mus muscu
1253	19	0.8	226891	2	AC120396	AC120396	Mus muscu
c1254	19	0.8	226891	2	AC120396	AC120396	Mus muscu
c1255	19	0.8	227401	2	AC106650	AC106650	Rattus no
c1256	19	0.8	227454	10	AC027700	AC027700	Mus muscu
c1257	19	0.8	227616	2	AC103525	AC103525	Rattus no

1258	19	0.8	227665	2	AC133323	AC133323	Rattus no
1259	19	0.8	227696	2	AC112936	AC112936	Mus muscu
c1260	19	0.8	228182	2	AC109615	AC109615	Mus muscu
c1261	19	0.8	228436	2	AC108544	AC108544	Rattus no
1262	19	0.8	228444	10	AL844147	AL844147	Mouse DNA
c1263	19	0.8	228508	5	AB102768	AB102768	Oryzias l
c1264	19	0.8	228752	2	AC094632	AC094632	Rattus no
1265	19	0.8	228947	2	AC111430	AC111430	Rattus no
1266	19	0.8	229212	2	AC114168	AC114168	Rattus no
c1267	19	0.8	229315	2	AC105651	AC105651	Rattus no
c1268	19	0.8	229548	2	AC106974	AC106974	Rattus no
c1269	19	0.8	229612	2	AL161647	AL161647	Homo sapi
1270	19	0.8	229661	2	AC124474	AC124474	Mus muscu
1271	19	0.8	229792	2	AC113825	AC113825	Rattus no
c1272	19	0.8	230067	2	AC095377	AC095377	Rattus no
1273	19	0.8	230417	2	AC120447	AC120447	Rattus no
1274	19	0.8	230659	2	AC150012	AC150012	Callithri
1275	19	0.8	231234	2	AC134014	AC134014	Rattus no
c1276	19	0.8	231303	5	BX649405	BX649405	Zebrafish
c1277	19	0.8	232184	2	AC103006	AC103006	Rattus no
c1278	19	0.8	232369	2	AC122598	AC122598	Rattus no
1279	19	0.8	233157	2	AC105468	AC105468	Rattus no
1280	19	0.8	233399	2	AC129412	AC129412	Rattus no
c1281	19	0.8	233924	10	AC134579	AC134579	Mus muscu
1282	19	0.8	233992	2	AC094047	AC094047	Rattus no
c1283	19	0.8	233997	2	AC128367	AC128367	Rattus no
c1284	19	0.8	233997	10	AL606521	AL606521	Mouse DNA
c1285	19	0.8	234009	2	CR383672	CR383672	Danio rer
1286	19	0.8	234047	2	AC096460	AC096460	Rattus no
c1287	19	0.8	234160	2	AC117890	AC117890	Rattus no
1288	19	0.8	234344	2	BX323797	BX323797	Danio rer
c1289	19	0.8	234518	2	AC107719	AC107719	Mus muscu
1290	19	0.8	234698	2	AC114581	AC114581	Mus muscu
1291	19	0.8	234939	2	AC094809	AC094809	Rattus no
c1292	19	0.8	235259	2	AC118945	AC118945	Rattus no
c1293	19	0.8	235547	2	AC112586	AC112586	Rattus no
1294	19	0.8	235638	2	AC097984	AC097984	Rattus no
1295	19	0.8	235652	2	AC123474	AC123474	Rattus no
c1296	19	0.8	236275	2	AC120624	AC120624	Rattus no
1297	19	0.8	236385	2	AC094936	AC094936	Rattus no
c1298	19	0.8	237082	10	AL671229	AL671229	Mouse DNA
c1299	19	0.8	237293	2	AC120666	AC120666	Rattus no
1300	19	0.8	237329	2	AC151386	AC151386	Callithri
c1301	19	0.8	237344	2	AC096256	AC096256	Rattus no
1302	19	0.8	237422	5	BX546500	BX546500	Zebrafish
1303	19	0.8	237569	5	BX649547	BX649547	Zebrafish
c1304	19	0.8	237581	2	AC131646	AC131646	Rattus no
c1305	19	0.8	237876	10	AC124601	AC124601	Mus muscu
1306	19	0.8	238046	2	AC109052	AC109052	Rattus no
c1307	19	0.8	238116	2	AC114050	AC114050	Rattus no
c1308	19	0.8	238478	2	AC133432	AC133432	Rattus no
c1309	19	0.8	238850	2	AC094265	AC094265	Rattus no
c1310	19	0.8	238877	2	AC115347	AC115347	Rattus no
1311	19	0.8	238973	2	AC133265	AC133265	Rattus no
1312	19	0.8	239029	2	AC127670	AC127670	Rattus no
1313	19	0.8	239054	2	AC139513	AC139513	Mus muscu
c1314	19	0.8	239113	2	AC094034	AC094034	Rattus no

c1315	19	0.8	239190	2	AC098990	AC098990	Rattus no
1316	19	0.8	239339	2	AC091703	AC091703	Mus muscu
1317	19	0.8	239946	2	AC103505	AC103505	Rattus no
c1318	19	0.8	240004	2	AC113960	AC113960	Mus muscu
1319	19	0.8	240093	2	AC112358	AC112358	Rattus no
1320	19	0.8	240272	2	AC097809	AC097809	Rattus no
c1321	19	0.8	241137	2	AC112078	AC112078	Rattus no
c1322	19	0.8	241199	2	AC105526	AC105526	Rattus no
1323	19	0.8	241418	2	AC098054	AC098054	Rattus no
1324	19	0.8	241616	10	AC129191	AC129191	Mus muscu
1325	19	0.8	241753	2	AC019149	AC019149	Homo sapi
1326	19	0.8	242347	10	AC107789	AC107789	Mus muscu
c1327	19	0.8	242739	2	AC106316	AC106316	Rattus no
1328	19	0.8	242820	2	AC093939	AC093939	Rattus no
1329	19	0.8	242832	10	AC117584	AC117584	Mus muscu
1330	19	0.8	243073	2	AC108537	AC108537	Rattus no
c1331	19	0.8	243124	2	AC097249	AC097249	Rattus no
1332	19	0.8	243422	2	AC098453	AC098453	Rattus no
1333	19	0.8	243556	2	AC114066	AC114066	Rattus no
1334	19	0.8	243804	2	AC136662	AC136662	Rattus no
1335	19	0.8	244050	2	AY657028	AY657028	Mus muscu
1336	19	0.8	244130	2	AC125658	AC125658	Rattus no
1337	19	0.8	244268	2	AC129795	AC129795	Rattus no
c1338	19	0.8	244278	2	AC094685	AC094685	Rattus no
1339	19	0.8	244573	2	AC133400	AC133400	Rattus no
1340	19	0.8	244675	2	AC094935	AC094935	Rattus no
1341	19	0.8	244693	2	AC132971	AC132971	Rattus no
1342	19	0.8	244721	2	AC107195	AC107195	Rattus no
c1343	19	0.8	245283	2	AC096351	AC096351	Rattus no
1344	19	0.8	246384	2	AC108543	AC108543	Rattus no
1345	19	0.8	246630	2	AC095178	AC095178	Rattus no
c1346	19	0.8	246886	2	AC108560	AC108560	Rattus no
c1347	19	0.8	247187	2	AC094928	AC094928	Rattus no
c1348	19	0.8	247208	2	AC120766	AC120766	Rattus no
1349	19	0.8	247451	2	AC097417	AC097417	Rattus no
1350	19	0.8	247936	2	AC112533	AC112533	Rattus no
1351	19	0.8	247961	10	AC016814	AC016814	Mus muscu
c1352	19	0.8	248329	2	AC109989	AC109989	Rattus no
1353	19	0.8	248379	2	AC110341	AC110341	Rattus no
1354	19	0.8	250169	2	AC126583	AC126583	Rattus no
1355	19	0.8	250353	10	AL590969	AL590969	Mouse DNA
1356	19	0.8	250586	2	AC126536	AC126536	Rattus no
1357	19	0.8	250999	2	AC119009	AC119009	Rattus no
1358	19	0.8	251050	5	BX323060	BX323060	Zebrafish
c1359	19	0.8	252148	2	AC127936	AC127936	Rattus no
c1360	19	0.8	253142	2	AC128641	AC128641	Rattus no
c1361	19	0.8	253148	2	AC098015	AC098015	Rattus no
1362	19	0.8	253297	2	AC134076	AC134076	Rattus no
1363	19	0.8	253474	2	AC095441	AC095441	Rattus no
c1364	19	0.8	253712	2	AC095520	AC095520	Rattus no
c1365	19	0.8	255924	2	AC096518	AC096518	Rattus no
1366	19	0.8	257396	2	AC130569	AC130569	Rattus no
c1367	19	0.8	257595	2	AC123011	AC123011	Rattus no
c1368	19	0.8	258847	2	AC112746	AC112746	Rattus no
1369	19	0.8	259123	2	AC108237	AC108237	Rattus no
1370	19	0.8	259720	2	AC094497	AC094497	Rattus no
1371	19	0.8	259762	2	AC102615	AC102615	Mus muscu

c1372	19	0.8	259970	2	AC106985	AC106985	Rattus no
1373	19	0.8	260241	2	AC105158	AC105158	Mus muscu
c1374	19	0.8	261498	2	AC073823	AC073823	Mus muscu
c1375	19	0.8	262032	2	AC131396	AC131396	Rattus no
1376	19	0.8	262050	2	AC105575	AC105575	Rattus no
1377	19	0.8	262124	2	AC095111	AC095111	Rattus no
1378	19	0.8	262142	2	AC095654	AC095654	Rattus no
c1379	19	0.8	263730	2	AC094314	AC094314	Rattus no
1380	19	0.8	263954	2	AC117122	AC117122	Rattus no
1381	19	0.8	264380	2	AC120824	AC120824	Rattus no
c1382	19	0.8	266926	2	AC112028	AC112028	Rattus no
1383	19	0.8	266973	2	AC109414	AC109414	Rattus no
c1384	19	0.8	267328	2	AC110688	AC110688	Rattus no
1385	19	0.8	267749	2	AC131472	AC131472	Rattus no
1386	19	0.8	267795	2	AC096390	AC096390	Rattus no
1387	19	0.8	268663	2	AC110147	AC110147	Rattus no
c1388	19	0.8	269229	2	AC097551	AC097551	Rattus no
1389	19	0.8	269301	2	AC102913	AC102913	Mus muscu
1390	19	0.8	270086	2	AC128132	AC128132	Rattus no
1391	19	0.8	270108	2	AC125642	AC125642	Rattus no
1392	19	0.8	271429	2	AC129086	AC129086	Rattus no
c1393	19	0.8	272336	2	AC128072	AC128072	Rattus no
1394	19	0.8	272698	3	PFMAL4P4	AL035477	Plasmodiu
1395	19	0.8	273413	2	AC079314	AC079314	Homo sapi
c1396	19	0.8	273715	2	AC140797	AC140797	Mus muscu
1397	19	0.8	273722	2	AC098260	AC098260	Rattus no
c1398	19	0.8	275111	2	AC115133	AC115133	Rattus no
1399	19	0.8	275900	2	AC103476	AC103476	Rattus no
1400	19	0.8	276787	2	AC113850	AC113850	Rattus no
c1401	19	0.8	277124	2	AC132639	AC132639	Rattus no
c1402	19	0.8	277196	9	AE014302	AE014302	Homo sapi
1403	19	0.8	277220	2	AC097838	AC097838	Rattus no
c1404	19	0.8	278206	2	AL513471	AL513471	Homo sapi
c1405	19	0.8	279232	2	AC120754	AC120754	Rattus no
c1406	19	0.8	282610	2	AC096244	AC096244	Rattus no
c1407	19	0.8	282788	2	AC120748	AC120748	Rattus no
c1408	19	0.8	286007	2	BX942834	BX942834	Danio rer
1409	19	0.8	286448	2	AC116760	AC116760	Mus muscu
1410	19	0.8	288728	2	AC099368	AC099368	Rattus no
c1411	19	0.8	289545	2	AC096832	AC096832	Rattus no
1412	19	0.8	289893	3	AE003576	AE003576	Drosophil
c1413	19	0.8	290029	1	AE017134	AE017134	Yersinia
1414	19	0.8	290128	2	AC124325	AC124325	Mus muscu
1415	19	0.8	296756	3	AE003492	AE003492	Drosophil
c1416	19	0.8	296756	3	AE003492	AE003492	Drosophil
c1417	19	0.8	297235	2	AL499603	AL499603	Homo sapi
c1418	19	0.8	297984	2	AC099152	AC099152	Rattus no
c1419	19	0.8	300000	9	AP002530	AP002530	Homo sapi
1420	19	0.8	300201	2	AC107086	AC107086	Rattus no
1421	19	0.8	300988	2	AC096249	AC096249	Rattus no
c1422	19	0.8	301450	1	AP003185	AP003185	Clostridi
1423	19	0.8	304230	1	AE016940	AE016940	Bacteroid
1424	19	0.8	305900	3	AE003590	AE003590	Drosophil
c1425	19	0.8	309662	2	AC004469	AC004469	Homo sapi
1426	19	0.8	313378	2	AC094200	AC094200	Rattus no
1427	19	0.8	318503	2	AC074166	AC074166	Mus muscu
c1428	19	0.8	319367	10	AC021709	AC021709	Mus muscu

1429	19	0.8	321250	1	MPULM02	AL445564	Mycoplasma
1430	19	0.8	322101	6	AX814520	AX814520	Sequence
c1431	19	0.8	329753	2	AC096701	AC096701	Rattus no
c1432	19	0.8	331448	2	AC134126	AC134126	Rattus no
c1433	19	0.8	334050	1	AJ414151	AJ414151	Yersinia
c1434	19	0.8	336609	1	BX571867	BX571867	Photobact
1435	19	0.8	336873	2	AC104875	AC104875	Mus muscu
1436	19	0.8	338197	2	AC151283	AC151283	Mus muscu
c1437	19	0.8	340000	9	HS21C084	AL163284	Homo sapi
1438	19	0.8	346357	1	BX842647	BX842647	Bdellovib
c1439	19	0.8	346542	2	AC120727	AC120727	Rattus no
c1440	19	0.8	347572	2	AC107303	AC107303	Homo sapi
1441	19	0.8	349080	1	CR378667	CR378667	Photobact
c1442	19	0.8	349980	6	CQ870214	CQ870214	Sequence
1443	19	0.8	349980	6	CQ870217	CQ870217	Sequence
1444	19	0.8	349980	6	AX571765	AX571765	Sequence
1445	19	0.8	349980	6	AX770905	AX770905	Sequence
1446	18	0.8	18	6	AX697385	AX697385	Sequence
1447	18	0.8	90	6	CQ809145	CQ809145	Sequence
c1448	18	0.8	100	6	AX989875	AX989875	Sequence
c1449	18	0.8	100	6	AX989876	AX989876	Sequence
1450	18	0.8	128	11	G31764	G31764	sWSS3153 Er
1451	18	0.8	189	6	CQ740741	CQ740741	Sequence
1452	18	0.8	189	11	BV101285	BV101285	RPAMSEQ0
1453	18	0.8	201	11	BV201536	BV201536	sqnm20683
1454	18	0.8	201	11	BV208102	BV208102	sqnm22547
1455	18	0.8	201	11	BV208103	BV208103	sqnm22547
1456	18	0.8	211	3	TRFKPB	M18394	C.fascicula
c1457	18	0.8	227	9	HUMMSP03	M34375	Homo sapien
c1458	18	0.8	250	3	MICFMNC3	X04483	Critidia fa
1459	18	0.8	269	3	CFKTAA	X66923	C.fascicula
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c1461	18	0.8	303	6	AR083938	AR083938	Sequence
c1462	18	0.8	303	9	AF113846	AF113846	Homo sapi
c1463	18	0.8	323	5	AY330910	AY330910	Scaphiupu
1464	18	0.8	333	6	CQ731579	CQ731579	Sequence
c1465	18	0.8	337	5	AF402880	AF402880	Acipenser
c1466	18	0.8	337	5	AF402881	AF402881	Acipenser
c1467	18	0.8	337	5	AF402882	AF402882	Acipenser
c1468	18	0.8	337	5	AF402883	AF402883	Acipenser
c1469	18	0.8	337	5	AF402884	AF402884	Acipenser
c1470	18	0.8	337	5	AF402885	AF402885	Acipenser
c1471	18	0.8	337	5	AF402886	AF402886	Acipenser
c1472	18	0.8	337	5	AF402887	AF402887	Acipenser
c1473	18	0.8	337	5	AF402888	AF402888	Acipenser
c1474	18	0.8	337	5	AF402889	AF402889	Acipenser
c1475	18	0.8	337	5	AF402890	AF402890	Acipenser
c1476	18	0.8	337	5	AF402891	AF402891	Acipenser
c1477	18	0.8	337	5	AF402892	AF402892	Acipenser
c1478	18	0.8	337	5	AF402893	AF402893	Acipenser
c1479	18	0.8	337	5	AF402894	AF402894	Acipenser
c1480	18	0.8	337	5	AF402895	AF402895	Acipenser
c1481	18	0.8	337	5	AF402896	AF402896	Huso daur
c1482	18	0.8	337	5	AF402897	AF402897	Huso huso
c1483	18	0.8	337	5	AF402898	AF402898	Pseudosca
c1484	18	0.8	337	5	AF402899	AF402899	Pseudosca
c1485	18	0.8	337	5	AF402900	AF402900	Scaphirhy

c1486	18	0.8	337	5	AF402901	AF402901 Scaphirhy
c1487	18	0.8	337	5	AF402902	AF402902 Scaphirhy
c1488	18	0.8	337	5	AF402903	AF402903 Polyodon
c1489	18	0.8	337	5	AF402904	AF402904 Psephurus
c1490	18	0.8	346	5	MTSH12S1	X86226 S.holbrooki
c1491	18	0.8	355	5	AY430247	AY430247 Scaphirhy
1492	18	0.8	358	4	AF511171	AF511171 Sus scrof
c1493	18	0.8	358	11	BV060954	BV060954 S212P6013
1494	18	0.8	361	6	BD059704	BD059704 Secreted
1495	18	0.8	376	11	G64820	G64820 B102I13.GSS
1496	18	0.8	386	11	AB165494	AB165494 Bos tauru
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c1498	18	0.8	391	5	ABU86710	U86710 Acipenser b
c1499	18	0.8	399	6	CQ459477	CQ459477 Sequence
1500	18	0.8	402	6	AX224134	AX224134 Sequence

ALIGNMENTS

RESULT 1

AX697213

LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 281 from Patent WO0078961.

ACCESSION AX697213

VERSION AX697213.1 GI:29498151

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 281 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1. .2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2320; DB 6; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA	1080
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Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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RESULT 2

AY358416

LOCUS AY358416 2320 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA, complete cds.

ACCESSION AY358416

VERSION AY358416.1 GI:37181956

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2320)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,

Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309

REFERENCE 2 (bases 1 to 2320)

AUTHORS Clark,H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

source 1. .2320
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gene 1. .2320
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ORIGIN

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280

Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 3

AX136141

LOCUS AX136141 2341 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 63 from Patent EP1067182.

ACCESSION AX136141

VERSION AX136141.1 GI:14272549

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 63 10-JAN-2001;
 Helix Research Institute (JP)

FEATURES Location/Qualifiers

source

1. .2341

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

CDS

94. .1665

/note="unnamed protein product"

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/protein_id="CAC39713.1"

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 PFVAILSTSFGSLEFGLPIPLSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQ
 STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPI
 KPVPQDLENFIAKFEDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQS
 HWP KDVHLAANVKIVDWLPQSDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfg
 DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS
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ORIGIN

Query Match 93.2%; Score 2162; DB 6; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTTAGA	60
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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	120
Db	87	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	146
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	147	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	206
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266
Qy	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	267	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	326
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGAATTTCTTCTGGA	360
Db	327	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGAATTTCTTCTGGA	386
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	447	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	506
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTGGGCTCTTGGAAATTTGGGCTACC	600
Db	567	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTGGGCTCTTGGAAATTTGGGCTACC	626
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660

Db	627	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	747	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	806
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1106
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTCACCACGGCGGGCAGAATAGCATAATGGAGGC	1226
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1227	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1347	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1406
Qy	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Db	1467	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1526

Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1707	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1766
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1826
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1827	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1886
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1887	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1946
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1947	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	2006
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	2007	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2066
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2067	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2126
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2127	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2186
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2187	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2246
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2247	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2306
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC	2315
Db	2307	AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC	2341

RESULT 4

BD123523

LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123523

VERSION BD123523.1 GI:23218468

KEYWORDS JP 2002017376-A/32.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2341)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002017376-A/32

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC

PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FH Key Location/Qualifiers

FT CDS (94)..(1662).

FEATURES Location/Qualifiers

source

1..2341

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 93.2%; Score 2162; DB 6; Length 2341;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Db 27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

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Db 87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

|||||

Db 147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTACCATGCTTAACCA 240

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Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266
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Db	267	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	326
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	327	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	386
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	447	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	506
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	567	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	626
Qy	601	AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	627	AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	747	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	806
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGTCTACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1080
Db	1047	TGCCTTTGTCTACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1106

Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1226
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1227	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1347	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1406
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1467	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1526
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1707	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1766
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1826
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1827	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1886
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1887	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1946

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 Db 2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066
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 Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2127 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Db 2247 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2306
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC 2315
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 Db 2307 AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC 2341
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RESULT 5

AK075383

LOCUS AK075383 2341 bp mRNA linear PRI 03-SEP-2002

DEFINITION Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).

ACCESSION AK075383

VERSION AK075383.1 GI:22761433

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2341)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986).

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University

Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Db	447	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	506
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC	600
Db	567	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC	626
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	627	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	747	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	806
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1106
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1226

Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1227	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1347	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1406
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1467	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1526
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1707	TCACCATTTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1766
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1826
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1827	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1886
Qy	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1920
Db	1887	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1946
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1947	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	2006
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	2007	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2066
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100

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Db      2067  |||||
          TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2126

Qy      2101  TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
          |||||

Db      2127  TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186

Qy      2161  AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
          |||||

Db      2187  AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2246

Qy      2221  CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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Db      2247  CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2306

Qy      2281  AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
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Db      2307  AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2341

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RESULT 6

AX548037

LOCUS AX548037 2944 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 13 from Patent WO02066654.

ACCESSION AX548037

VERSION AX548037.1 GI:25813133

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,
Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,
Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,
Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 02066654-A 13 29-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .2944

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="Incyte ID No: 7486594CB1"

ORIGIN

Query Match 84.4%; Score 1957; DB 6; Length 2944;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2057; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      262  AGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCA 321
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Db      363  AGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCA 422

Qy      322  TCAAAGAGAATTTAAAAAGAGTTTGTATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGG 381
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Db	423	TCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGG	482
Qy	382	AAAATTTGAAAAC TTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTT	441
Db	483	AAAATTTGAAAAC TTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTT	542
Qy	442	AAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGA	501
Db	543	AAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGA	602
Qy	502	AACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCAT	561
Db	603	AACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCAT	662
Qy	562	TCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCC	621
Db	663	TCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCC	722
Qy	622	AGTATTCGGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCT	681
Db	723	AGTATTCGGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCT	782
Qy	682	GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCAT	741
Db	783	GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCAT	842
Qy	742	CAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGA	801
Db	843	CAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGA	902
Qy	802	GTTGTGGTTTCATTAAC TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACAC	861
Db	903	GTTGTGGTTTCATTAAC TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACAC	962
Qy	862	TGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAA	921
Db	963	TGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAA	1022
Qy	922	CTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAA	981
Db	1023	CTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAA	1082
Qy	982	CACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCA	1041
Db	1083	CACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCA	1142
Qy	1042	AGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAA	1101
Db	1143	AGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAA	1202
Qy	1102	TGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCT	1161
Db	1203	TGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCT	1262
Qy	1162	GTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCAT	1221
Db	1263	GTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCAT	1322

Qy	1222	GGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAA	1281
Db	1323	GGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAA	1382
Qy	1282	GTTTGGTGTTTCTATTCAAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAA	1341
Db	1383	GTTTGGTGTTTCTATTCAAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAA	1442
Qy	1342	ACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTATCCTGCG	1401
Db	1443	ACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTATCCTGCG	1502
Qy	1402	CTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGAC	1461
Db	1503	CTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGAC	1562
Qy	1462	AGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCT	1521
Db	1563	AGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCT	1622
Qy	1522	GTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAA	1581
Db	1623	GTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAA	1682
Qy	1582	GCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGG	1641
Db	1683	GCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGG	1742
Qy	1642	CCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTC	1701
Db	1743	CCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTC	1802
Qy	1702	CCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGA	1761
Db	1803	CCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGA	1862
Qy	1762	ACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCT	1821
Db	1863	ACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCT	1922
Qy	1822	TACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCA	1881
Db	1923	TACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCA	1982
Qy	1882	TCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATT	1941
Db	1983	TCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATT	2042
Qy	1942	TCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTC	2001
Db	2043	TCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTC	2102
Qy	2002	CAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGG	2061
Db	2103	CAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGG	2162

Qy 2062 AATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACAT 2121
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 Db 2163 AATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACAT 2222
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 Qy 2122 ATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGC 2181
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 Db 2223 ATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGC 2282
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 Db 2283 TCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTG 2342
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 Qy 2242 AGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTAT 2301
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 Db 2343 AGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTAT 2402
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 Qy 2302 CTCTCCCCAACCTCACTAA 2320
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 Db 2403 CTCTCCCCAACCTCACTAA 2421
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RESULT 7
 CQ726650

LOCUS CQ726650 1836 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 12584 from Patent WO02068579.

ACCESSION CQ726650

VERSION CQ726650.1 GI:42290368

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of
 human exons or transcripts, for detecting expression and other uses
 thereof

JOURNAL Patent: WO 02068579-A 12584 06-SEP-2002;
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers
 source 1. .1836
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 39.0%; Score 905; DB 6; Length 1836;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 577
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 Db 61 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 120
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Qy	578	GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTG	637
Db	121	GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTG	180
Qy	638	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	697
Db	181	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	240
Qy	698	TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTACA	757
Db	241	TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTACA	300
Qy	758	GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC	817
Db	301	GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC	360
Qy	818	TCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC	877
Db	361	TCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC	420
Qy	878	TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT	937
Db	421	TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT	480
Qy	938	GGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCG	997
Db	481	GGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCG	540
Qy	998	GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG	1057
Db	541	GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG	600
Qy	1058	TGTCAGTGTTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC	1117
Db	601	TGTCAGTGTTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC	660
Qy	1118	TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGC	1177
Db	661	TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGC	720
Qy	1178	GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC	1237
Db	721	GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC	780
Qy	1238	TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATT	1297
Db	781	TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATT	840
Qy	1298	CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC	1357
Db	841	CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC	900
Qy	1358	AAGAG	1362
Db	901	AAGAG	905

RESULT 8

AC008947/c

LOCUS AC008947 88948 bp DNA linear HTG 05-MAY-2000

DEFINITION Homo sapiens chromosome 5 clone CTD-2330L9, WORKING DRAFT SEQUENCE,
19 unordered pieces.

ACCESSION AC008947

VERSION AC008947.5 GI:7710868

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 88948)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 5

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 88948)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On May 5, 2000 this sequence version replaced gi:6997051.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 754542

Center clone name: CITB-H1_2330L9

Summary Statistics

Consensus quality: 67454 bases at least Q40

Consensus quality: 80777 bases at least Q30

Consensus quality: 83103 bases at least Q20

Estimated insert size: 85000; pulse field gel estimation

Estimated insert size: 87148; sum-of-contigs estimation

Quality coverage: 3.94 in Q20 bases; pulse field gel estimation

Quality coverage: 3.84 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2375: contig of 2375 bp in length

* 2376 2475: gap of unknown length

* 2476 5577: contig of 3102 bp in length

* 5578 5677: gap of unknown length

* 5678 7838: contig of 2161 bp in length

* 7839 7938: gap of unknown length

* 7939 10123: contig of 2185 bp in length

* 10124 10223: gap of unknown length

* 10224 12755: contig of 2532 bp in length

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* 12756 12855: gap of unknown length
* 12856 15242: contig of 2387 bp in length
* 15243 15342: gap of unknown length
* 15343 17589: contig of 2247 bp in length
* 17590 17689: gap of unknown length
* 17690 20485: contig of 2796 bp in length
* 20486 20585: gap of unknown length
* 20586 23628: contig of 3043 bp in length
* 23629 23728: gap of unknown length
* 23729 26745: contig of 3017 bp in length
* 26746 26845: gap of unknown length
* 26846 30194: contig of 3349 bp in length
* 30195 30294: gap of unknown length
* 30295 34563: contig of 4269 bp in length
* 34564 34663: gap of unknown length
* 34664 39707: contig of 5044 bp in length
* 39708 39807: gap of unknown length
* 39808 47134: contig of 7327 bp in length
* 47135 47234: gap of unknown length
* 47235 52767: contig of 5533 bp in length
* 52768 52867: gap of unknown length
* 52868 59030: contig of 6163 bp in length
* 59031 59130: gap of unknown length
* 59131 65592: contig of 6462 bp in length
* 65593 65692: gap of unknown length
* 65693 75313: contig of 9621 bp in length
* 75314 75413: gap of unknown length
* 75414 88948: contig of 13535 bp in length.

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FEATURES
source

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Location/Qualifiers
1. .88948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN

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Query Match          34.8%;  Score 807;  DB 2;  Length 88948;
Best Local Similarity 99.7%;  Pred. No. 0;
Matches 957;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

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Db      4580 AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCC 4521
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Qy      1421 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 1480
          |||
Db      4520 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 4461
          |||

Qy      1481 AAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTT 1540
          |||
Db      4460 AAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTT 4401
          |||

Qy      1541 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 1600
          |||
Db      4400 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 4341
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```

Qy	1601	TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG	1660
Db	4340	TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG	4281
Qy	1661	GGTCTGTTTGGTGGGCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC	1720
Db	4280	GGTCTGTTTGGTGGGCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC	4221
Qy	1721	CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA	1780
Db	4220	CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA	4161
Qy	1781	ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA	1840
Db	4160	ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA	4101
Qy	1841	GCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT	1900
Db	4100	GCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT	4041
Qy	1901	GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC	1960
Db	4040	GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC	3981
Qy	1961	TTCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC	2020
Db	3980	TTCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC	3921
Qy	2021	TAGTCAGCCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC	2080
Db	3920	TAGTCAGCCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC	3861
Qy	2081	ACCTTGCCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGG	2140
Db	3860	ACCTTGCCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGG	3801
Qy	2141	AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG	2200
Db	3800	AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG	3741
Qy	2201	GTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA	2260
Db	3740	GTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA	3681
Qy	2261	GGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCAACCTCACTAA	2320
Db	3680	GGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCAACCTCACTAA	3621

RESULT 9

AC016612

LOCUS AC016612 179513 bp DNA linear PRI 06-SEP-2001

DEFINITION Homo sapiens chromosome 5 clone CTD-2197M16, complete sequence.

ACCESSION AC016612

VERSION AC016612.6 GI:15451670

KEYWORDS HTG.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179513)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179513)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 179513)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (20-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 179513)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA

COMMENT On Sep 6, 2001 this sequence version replaced gi:11908274.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.4% of Sequence;
 Estimated Total Number of Errors is 0.8.
 STS Content:
 SHGC-141485 G63682
 SHGC-104791 G58536.

FEATURES Location/Qualifiers
 source 1. .179513
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTD-2197M16"

ORIGIN

Query Match 34.8%; Score 807; DB 9; Length 179513;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1361	AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCC	1420
Db	48084	AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCC	48143
Qy	1421	ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC	1480
Db	48144	ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC	48203
Qy	1481	AAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTT	1540
Db	48204	AAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTT	48263

Qy	1541	CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC	1600
Db	48264	CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC	48323
Qy	1601	TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG	1660
Db	48324	TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG	48383
Qy	1661	GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCC	1720
Db	48384	GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCC	48443
Qy	1721	CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA	1780
Db	48444	CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA	48503
Qy	1781	ATCATCCTTTCCACTTGCTAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTA	1840
Db	48504	ATCATCCTTTCCACTTGCTAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTA	48563
Qy	1841	GCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT	1900
Db	48564	GCAGAAATCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT	48623
Qy	1901	GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC	1960
Db	48624	GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC	48683
Qy	1961	TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC	2020
Db	48684	TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC	48743
Qy	2021	TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC	2080
Db	48744	TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC	48803
Qy	2081	ACCTTGCCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTTTCAATGCTCAGG	2140
Db	48804	ACCTTGCCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTTTCAATGCTCAGG	48863
Qy	2141	AAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG	2200
Db	48864	AAGCCTGCCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG	48923
Qy	2201	GTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA	2260
Db	48924	GTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA	48983
Qy	2261	GGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	48984	GGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	49043

RESULT 10

AX958403

LOCUS AX958403 2263 bp DNA linear PAT 14-JAN-2004

DEFINITION Sequence 31 from Patent WO0226988.
 ACCESSION AX958403
 VERSION AX958403.1 GI:40879361
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS .
 TITLE Human drug metabolizing enzymes
 JOURNAL Patent: WO 0226988-A 31 04-APR-2002;
 Incyte Genomics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. .2263
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 33.4%; Score 776; DB 6; Length 2263;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 826; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	968	GGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT	1027
Db	983	GGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT	1042
Qy	1028	GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTTCATTGGCCCAAAGATGTC	1087
Db	1043	GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTTCATTGGCCCAAAGATGTC	1102
Qy	1088	CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC	1147
Db	1103	CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC	1162
Qy	1148	CCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG	1207
Db	1163	CCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG	1222
Qy	1208	CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA	1267
Db	1223	CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA	1282
Qy	1268	GTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGAGACATTG	1327
Db	1283	GTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGAGACATTG	1342
Qy	1328	GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC	1387
Db	1343	GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC	1402
Qy	1388	AGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC	1447
Db	1403	AGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC	1462
Qy	1448	CACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGG	1507

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Db      1463 CACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCAGCCCTGG 1522
Qy      1508 CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1567
      |||
Db      1523 CATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1582
Qy      1568 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1627
      |||
Db      1583 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1642
Qy      1628 AAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCAT 1687
      |||
Db      1643 AAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCAT 1702
Qy      1688 TTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCC 1747
      |||
Db      1703 TTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCC 1762
Qy      1748 TGTTCCTTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1794
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Db      1763 TGTTCCTTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1809

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RESULT 11

AC025476/c

LOCUS AC025476 148069 bp DNA linear HTG 31-AUG-2001

DEFINITION Homo sapiens chromosome 5 clone RP11-36A10, WORKING DRAFT SEQUENCE;
4 unordered pieces.

ACCESSION AC025476

VERSION AC025476.5 GI:15290368

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 148069)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 5

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 148069)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Aug 25, 2001 this sequence version replaced gi:13699663.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 420199

Center clone name: RPCI-11_36A10

Summary Statistics

Consensus quality: 145481 bases at least Q40

Consensus quality: 147102 bases at least Q30
Consensus quality: 147415 bases at least Q20
Estimated insert size: 147360; agarose-fp estimation
Estimated insert size: 147769; sum-of-contigs estimation
Quality coverage: 5.89 in Q20 bases; agarose-fp estimation
Quality coverage: 5.88 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 8195: contig of 8195 bp in length
* 8196 8295: gap of unknown length
* 8296 35863: contig of 27568 bp in length
* 35864 35963: gap of unknown length
* 35964 86799: contig of 50836 bp in length
* 86800 86899: gap of unknown length
* 86900 148069: contig of 61170 bp in length.

FEATURES

source

Location/Qualifiers

1. .148069

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-36A10"

/clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 23.1%; Score 536; DB 2; Length 148069;

Best Local Similarity 100.0%; Pred. No. 8.7e-296;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      376 CAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAACTTGGCGTTGCAGTGCAGTCA 435
          |||
Db      16111 CAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAACTTGGCGTTGCAGTGCAGTCA 16052

Qy      436 TTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGAT 495
          |||
Db      16051 TTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGAT 15992

Qy      496 AGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGT 555
          |||
Db      15991 AGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGT 15932

Qy      556 GGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTA 615
          |||
Db      15931 GGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTA 15872

Qy      616 TGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAA 675
          |||
Db      15871 TGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAA 15812

Qy      676 TTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAA 735
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Db 15811 TTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAA 15752

Qy 736 CACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAA 795
 |||

Db 15751 CACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAA 15692

Qy 796 AGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCC 855
 |||

Db 15691 AGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCC 15632

Qy 856 CAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACAGTACCACAAG 911
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Db 15631 CAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACAGTACCACAAG 15576

RESULT 12

AX136632/c

LOCUS AX136632 594 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 554 from Patent EP1067182.

ACCESSION AX136632

VERSION AX136632.1 GI:14273036

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 554 10-JAN-2001;
 Helix Research Institute (JP)

FEATURES Location/Qualifiers

source 1. .594
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 20.2%; Score 468; DB 6; Length 594;

Best Local Similarity 100.0%; Pred. No. 1.4e-256;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1848 TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 1907
 |||

Db 468 TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 409

Qy 1908 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTC 1967
 |||

Db 408 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTC 349

Qy 1968 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 2027
 |||

Db 348 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 289

Qy 2028 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 2087
 |||

Db 288 CCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 229

Qy 2088 ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG 2147
 |||

Db 228 ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG 169

Qy 2148 CCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 2207
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Db 168 CCCTGTGCTTGAGAGTTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 109

Qy 2208 TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 2267
 |||

Db 108 TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 49

Qy 2268 AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
 |||

Db 48 AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 1

RESULT 13

BD123872/c

LOCUS BD123872 594 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123872

VERSION BD123872.1 GI:23218817

KEYWORDS JP 2002017376-A/381.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 594)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 381 22-JAN-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002017376-A/381

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
 10,

PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FH Key Location/Qualifiers

FT source 1. .594

FT /organism='Homo sapiens (human)'. .

FEATURES Location/Qualifiers

source 1. .594

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 20.2%; Score 468; DB 6; Length 594;
 Best Local Similarity 100.0%; Pred. No. 1.4e-256;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1848 TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 1907
          |||
Db      468 TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 409

Qy      1908 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTC 1967
          |||
Db      408 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTC 349

Qy      1968 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 2027
          |||
Db      348 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 289

Qy      2028 CCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 2087
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Db      288 CCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 229

Qy      2088 ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG 2147
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Db      228 ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG 169

Qy      2148 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 2207
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Db      168 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 109

Qy      2208 TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 2267
          |||
Db      108 TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 49

Qy      2268 AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
          |||
Db      48 AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 1
  
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RESULT 14

AC022136

LOCUS AC022136 125145 bp DNA linear HTG 06-MAY-2000

DEFINITION Homo sapiens chromosome 5 clone CTD-2221K22, WORKING DRAFT
 SEQUENCE, 37 unordered pieces.

ACCESSION AC022136

VERSION AC022136.3 GI:7711710

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 125145)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 5

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 125145)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL
COMMENT

Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On May 6, 2000 this sequence version replaced gi:7239447.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 712675

Center clone name: CITB-H1_2221K22

Summary Statistics

Consensus quality: 93614 bases at least Q40

Consensus quality: 109475 bases at least Q30

Consensus quality: 112774 bases at least Q20

Estimated insert size: 97000; pulse field gel estimation

Estimated insert size: 121545; sum-of-contigs estimation

Quality coverage: 5.83 in Q20 bases; pulse field gel estimation

Quality coverage: 4.65 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 37 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 2572: contig of 2572 bp in length

* 2573 2672: gap of unknown length

* 2673 4770: contig of 2098 bp in length

* 4771 4870: gap of unknown length

* 4871 7164: contig of 2294 bp in length

* 7165 7264: gap of unknown length

* 7265 9449: contig of 2185 bp in length

* 9450 9549: gap of unknown length

* 9550 12367: contig of 2818 bp in length

* 12368 12467: gap of unknown length

* 12468 14902: contig of 2435 bp in length

* 14903 15002: gap of unknown length

* 15003 17643: contig of 2641 bp in length

* 17644 17743: gap of unknown length

* 17744 20541: contig of 2798 bp in length

* 20542 20641: gap of unknown length

* 20642 22879: contig of 2238 bp in length

* 22880 22979: gap of unknown length

* 22980 25050: contig of 2071 bp in length

* 25051 25150: gap of unknown length

* 25151 27710: contig of 2560 bp in length

* 27711 27810: gap of unknown length

* 27811 30269: contig of 2459 bp in length

* 30270 30369: gap of unknown length

* 30370 32584: contig of 2215 bp in length

* 32585 32684: gap of unknown length

* 32685 35719: contig of 3035 bp in length

* 35720 35819: gap of unknown length

* 35820 38323: contig of 2504 bp in length

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* 38324 38423: gap of unknown length
* 38424 41441: contig of 3018 bp in length
* 41442 41541: gap of unknown length
* 41542 44320: contig of 2779 bp in length
* 44321 44420: gap of unknown length
* 44421 47540: contig of 3120 bp in length
* 47541 47640: gap of unknown length
* 47641 49926: contig of 2286 bp in length
* 49927 50026: gap of unknown length
* 50027 52948: contig of 2922 bp in length
* 52949 53048: gap of unknown length
* 53049 55882: contig of 2834 bp in length
* 55883 55982: gap of unknown length
* 55983 59431: contig of 3449 bp in length
* 59432 59531: gap of unknown length
* 59532 62545: contig of 3014 bp in length
* 62546 62645: gap of unknown length
* 62646 65729: contig of 3084 bp in length
* 65730 65829: gap of unknown length
* 65830 69494: contig of 3665 bp in length
* 69495 69594: gap of unknown length
* 69595 73457: contig of 3863 bp in length
* 73458 73557: gap of unknown length
* 73558 76848: contig of 3291 bp in length
* 76849 76948: gap of unknown length
* 76949 81440: contig of 4492 bp in length
* 81441 81540: gap of unknown length
* 81541 84401: contig of 2861 bp in length
* 84402 84501: gap of unknown length
* 84502 87615: contig of 3114 bp in length
* 87616 87715: gap of unknown length
* 87716 90814: contig of 3099 bp in length
* 90815 90914: gap of unknown length
* 90915 94882: contig of 3968 bp in length
* 94883 94982: gap of unknown length
* 94983 99188: contig of 4206 bp in length
* 99189 99288: gap of unknown length
* 99289 104355: contig of 5067 bp in length
* 104356 104455: gap of unknown length
* 104456 110393: contig of 5938 bp in length
* 110394 110493: gap of unknown length
* 110494 116770: contig of 6277 bp in length
* 116771 116870: gap of unknown length
* 116871 125145: contig of 8275 bp in length.

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FEATURES

source

Location/Qualifiers

1. .125145

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTD-2221K22"

/clone_lib="CalTech human BAC library D"

ORIGIN

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Query Match          18.2%;  Score 422;  DB 2;  Length 125145;
Best Local Similarity 99.8%;  Pred. No. 3.4e-230;
Matches 472;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy	1848	TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG	1907
Db	5002	TCTTTCCAGTCCTCTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG	5061
Qy	1908	TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC	1967
Db	5062	TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC	5121
Qy	1968	TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG	2027
Db	5122	TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG	5181
Qy	2028	CCTCTCTCACTCCTGCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC	2087
Db	5182	CCTCTCTCACTCCTGCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC	5241
Qy	2088	ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG	2147
Db	5242	ATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTG	5301
Qy	2148	CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG	2207
Db	5302	CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG	5361
Qy	2208	TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC	2267
Db	5362	TCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC	5421
Qy	2268	AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	5422	AGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	5474

RESULT 15

AR541778

LOCUS AR541778 2426 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 26 from patent US 6743619.

ACCESSION AR541778

VERSION AR541778.1 GI:53933858

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2426)

AUTHORS Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F., Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R., Wang,D. and Drmanac,R.T.

TITLE Nucleic acids and polypeptides

JOURNAL Patent: US 6743619-A 26 01-JUN-2004;

FEATURES Location/Qualifiers

source 1. .2426

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e-119;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGT 60

Qy      2107 TTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA 120

Qy      2167 GGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGA 180

Qy      2227 GCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCT 2276
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Db      181 GCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCT 230
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Search completed: March 25, 2005, 14:36:45
Job time : 9908 secs

GenCore version 5.1.6

Run on: March 25, 2005, 08:49:37 ; Search time 1161 Seconds
(without alignments)
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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- 3: geneseqn2000s:*
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- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AAC58107	standard; cDNA; 2320 BP.			
DE	Human PRO1780	nucleotide sequence SEQ ID NO:12.			
PN	WO200053750-A1.				
PD	14-SEP-2000.				
PA	(GETH) GENENTECH INC.				
	Query Match	100.0%;	Score 2320;	DB 3;	Length 2320;
	Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 2					
ID	AAA37101	standard; cDNA; 2320 BP.			
DE	Human PRO1780 (UNQ842)	cDNA sequence SEQ ID NO:281.			
PN	WO200012708-A2.				
PD	09-MAR-2000.				
PA	(GETH) GENENTECH INC.				
	Query Match	100.0%;	Score 2320;	DB 3;	Length 2320;
	Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 3					
ID	AAF54401	standard; DNA; 2320 BP.			
DE	Primer #82	used in the identification of proteins.			
PN	WO200078961-A1.				
PD	28-DEC-2000.				
PA	(GETH) GENENTECH INC.				
	Query Match	100.0%;	Score 2320;	DB 4;	Length 2320;
	Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 4					

ID ACD68440 standard; cDNA; 2320 BP.
DE Novel human secreted and transmembrane protein PRO1780 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID ACH04542 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ACD68086 standard; cDNA; 2320 BP.
DE Novel human secreted and transmembrane protein PRO1780 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID ADC18150 standard; cDNA; 2320 BP.
DE Human PRO polynucleotide #80.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID ADD70796 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ADD39873 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID ADD70319 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ADD38440 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ADD39396 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ADD38919 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID ADD40350 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 15

ID ADE50571 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 16

ID ADE20183 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 17

ID ADE50094 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 18

ID ADE21652 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 19
 ID ADF30077 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 20
 ID ADF55970 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 21
 ID ADH99474 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 22
 ID ADE96654 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 23
 ID ADF25965 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 24
 ID ADF24864 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 25
 ID ADF29600 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003203401-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 26

ID ADE97131 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003195334-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 27

ID ADH03169 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003216562-A1.
PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 28

ID ADH04123 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003220471-A1.
PD 27-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 29

ID ADH03646 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003224478-A1.
PD 04-DEC-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 30

ID ADH04600 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004005626-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 31

ID ADH61601 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004014130-A1.
PD 22-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 32

ID ADL94800 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004073015-A1.
PD 15-APR-2004.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 33
 ID AAF93775 standard; cDNA; 2341 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0073.
 PN EP1067182-A2.
 PD 10-JAN-2001.

PA (HELI-) HELIX RES INST.
 Query Match 93.2%; Score 2162; DB 5; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;

RESULT 34
 ID AAL41485 standard; DNA; 2944 BP.
 DE Drug metabolising enzyme encoding DNA - 7486594CB1.
 PN WO200266654-A2.
 PD 29-AUG-2002.

PA (INCY-) INCYTE GENOMICS INC.
 Query Match 84.4%; Score 1957; DB 6; Length 2944;
 Best Local Similarity 99.9%; Pred. No. 0;

RESULT 35
 ID AAS62475 standard; cDNA; 2074 BP.
 DE cDNA sequence #262 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.

PA (GEMY) GENETICS INST INC.
 Query Match 74.0%; Score 1717; DB 6; Length 2074;
 Best Local Similarity 99.7%; Pred. No. 0;

RESULT 36
 ID ADR19692 standard; DNA; 2263 BP.
 DE Human drug metabolising enzyme (DME)-13 gene sequence.
 PN WO200226988-A2.
 PD 04-APR-2002.

PA (INCY-) INCYTE GENOMICS INC.
 Query Match 33.4%; Score 776; DB 7; Length 2263;
 Best Local Similarity 99.9%; Pred. No. 0;

RESULT 37
 ID ABA09537 standard; cDNA; 1898 BP.
 DE Human PRO1780 homologue-encoding cDNA, SEQ ID NO:1313.
 PN WO200157188-A2.
 PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 25.5%; Score 591; DB 4; Length 1898;
 Best Local Similarity 99.8%; Pred. No. 9.5e-282;

RESULT 38
 ID AAS81804 standard; cDNA; 2220 BP.
 DE DNA encoding novel human diagnostic protein #17608.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 20.9%; Score 484; DB 5; Length 2220;
 Best Local Similarity 100.0%; Pred. No. 9.9e-229;

RESULT 39
 ID AAF94120 standard; DNA; 594 BP.
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 554.
 PN EP1067182-A2.
 PD 10-JAN-2001.

PA (HELI-) HELIX RES INST.

Query Match 20.2%; Score 468; DB 5; Length 594;
 Best Local Similarity 100.0%; Pred. No. 8e-221;
 RESULT 40
 ID ADN39359 standard; cDNA; 923 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B43.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 19.0%; Score 441; DB 11; Length 923;
 Best Local Similarity 100.0%; Pred. No. 1.9e-207;
 RESULT 41
 ID AAS84832 standard; cDNA; 2721 BP.
 DE DNA encoding novel human diagnostic protein #20636.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 17.5%; Score 407; DB 5; Length 2721;
 Best Local Similarity 100.0%; Pred. No. 1.4e-190;
 RESULT 42
 ID ABX70800 standard; cDNA; 2426 BP.
 DE Novel human cDNA sequence #25.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 PA (GOOD/) GOODRICH R W.
 Query Match 9.9%; Score 230; DB 8; Length 2426;
 Best Local Similarity 100.0%; Pred. No. 7e-103;
 RESULT 43
 ID AAS84831 standard; cDNA; 1242 BP.
 DE DNA encoding novel human diagnostic protein #20635.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.7%; Score 224; DB 5; Length 1242;
 Best Local Similarity 100.0%; Pred. No. 6.5e-100;
 RESULT 44
 ID AAS82074 standard; cDNA; 1242 BP.
 DE DNA encoding novel human diagnostic protein #17878.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.7%; Score 224; DB 5; Length 1242;
 Best Local Similarity 100.0%; Pred. No. 6.5e-100;
 RESULT 45
 ID AAF93971 standard; DNA; 770 BP.
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 405.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 6.0%; Score 139; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 8.3e-58;
 RESULT 46
 ID AAS81803 standard; cDNA; 659 BP.
 DE DNA encoding novel human diagnostic protein #17607.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 68; DB 5; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
RESULT 47
ID ABL57725 standard; DNA; 1182 BP.
DE Human sbg10054OUDPGT gene #1.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.

Query Match 2.9%; Score 68; DB 6; Length 1182;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 48
ID ABL57726 standard; DNA; 1572 BP.
DE Human sbg10054OUDPGT gene #2.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.

Query Match 2.9%; Score 68; DB 6; Length 1572;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 49
ID ABK90831 standard; cDNA; 1851 BP.
DE cDNA encoding drug metabolising enzyme.
PN US2002082194-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.

Query Match 2.9%; Score 68; DB 6; Length 1851;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 50
ID AAD24667 standard; cDNA; 2086 BP.
DE Human drug metabolising enzyme (DME)-2 cDNA.
PN WO200179468-A2.
PD 25-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.9%; Score 68; DB 6; Length 2086;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 51
ID ADA21188 standard; cDNA; 2268 BP.
DE Human secreted protein SECP-42 encoding cDNA SEQ ID NO:93.
PN WO2003068943-A2.
PD 21-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.9%; Score 68; DB 9; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 52
ID ADQ75567 standard; cDNA; 2791 BP.
DE Uridine diphosphate-galactosyl ceramide glucuronyl collagen transferase.
PN CN1380409-A.
PD 20-NOV-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Query Match 2.9%; Score 68; DB 11; Length 2791;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 RESULT 53
 ID AAD06821 standard; cDNA; 2797 BP.
 DE Human secreted protein Zalpha37 cDNA.
 PN WO200138505-A2.
 PD 31-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 2.9%; Score 68; DB 4; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 RESULT 54
 ID ADA53720 standard; cDNA; 2823 BP.
 DE Human coding sequence, SEQ ID 1288.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 2.9%; Score 68; DB 10; Length 2823;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 RESULT 55
 ID ADQ64368 standard; cDNA; 5002 BP.
 DE Novel human cDNA sequence #1529.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 2.9%; Score 68; DB 12; Length 5002;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 RESULT 56
 ID ABK90832 standard; DNA; 42999 BP.
 DE Genomic DNA encoding drug metabolising enzyme.
 PN US2002082194-A1.
 PD 27-JUN-2002.
 PA (GUEG/) GUEGLER K.
 PA (WEBS/) WEBSTER M.
 PA (YANC/) YAN C.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 2.9%; Score 68; DB 6; Length 42999;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 RESULT 57
 ID AAD25345 standard; cDNA; 2082 BP.
 DE Human UDP-glycosyltransferase, 32626 cDNA.
 PN WO200202774-A2.
 PD 10-JAN-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 2.4%; Score 55; DB 6; Length 2082;
 Best Local Similarity 100.0%; Pred. No. 3.6e-16;
 RESULT 58
 ID ADN02571 standard; DNA; 2868 BP.
 DE Human hepatouracil dinucleotide glycosyltransferase 29.7 DNA.
 PN CN1393551-A.
 PD 29-JAN-2003.
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 Query Match 2.4%; Score 55; DB 11; Length 2868;
 Best Local Similarity 100.0%; Pred. No. 3.6e-16;
 RESULT 59
 ID ADB62657 standard; cDNA; 1842 BP.
 DE Human cDNA encoding clone KIDNE20186170.

PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 2.2%; Score 52; DB 10; Length 1842;
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 RESULT 60
 ID AAC58024 standard; DNA; 45 BP.
 DE Human PRO1780 hybridisation probe SEQ ID NO:16.
 PN WO200053750-A1.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 3; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 61
 ID AAA37270 standard; DNA; 45 BP.
 DE Human PRO1780 hybridisation probe SEQ ID NO:285.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 3; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 62
 ID AAF54404 standard; DNA; 45 BP.
 DE Primer #83 used in the identification of proteins.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 63
 ID ACD68443 standard; DNA; 45 BP.
 DE Novel human secreted and transmembrane protein related probe #41.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 64
 ID ACH04545 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 65
 ID ACD68089 standard; DNA; 45 BP.
 DE Novel human secreted and transmembrane protein related probe #41.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 66
 ID ADC18154 standard; DNA; 45 BP.
 DE Human PRO probe #41.

PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 67
ID ADD70800 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 68
ID ADD39877 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 69
ID ADD70323 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 70
ID ADD38444 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 71
ID ADD39400 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 72
ID ADD38923 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 73
ID ADD40354 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082627-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 74
 ID ADE50575 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 75
 ID ADE20187 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 76
 ID ADE50098 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 77
 ID ADE21656 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 78
 ID ADF30081 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 79
 ID ADF55974 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 80
 ID ADH99478 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003065142-A1.
 PD 03-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 81
 ID ADE96658 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003195347-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 82
 ID ADF25969 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003199675-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 83
 ID ADF24868 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003198993-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 84
 ID ADF29604 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003203401-A1.
 PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 85
 ID ADE97135 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003195334-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 86
 ID ADH03173 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003216562-A1.
 PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;

RESULT 87
 ID ADH04127 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003220471-A1.
 PD 27-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 88
 ID ADH03650 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 89
 ID ADH04604 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 90
 ID ADH61605 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 91
 ID ADL94804 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 RESULT 92
 ID AAL05664 standard; DNA; 5973 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8352.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.9%; Score 45; DB 4; Length 5973;
 Best Local Similarity 100.0%; Pred. No. 3.3e-11;
 RESULT 93
 ID AAL05665 standard; DNA; 5974 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8353.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.9%; Score 45; DB 4; Length 5974;
 Best Local Similarity 100.0%; Pred. No. 3.3e-11;
 RESULT 94
 ID ACN45086 standard; DNA; 54493 BP.
 DE Human genomic sequence hCG37578.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.3%; Score 30; DB 11; Length 54493;

Best Local Similarity 100.0%; Pred. No. 0.00097;

RESULT 95

ID AAK24438 standard; DNA; 277 BP.

DE Human brain expressed single exon probe SEQ ID NO: 24429.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.2%; Score 29; DB 4; Length 277;

Best Local Similarity 100.0%; Pred. No. 0.0026;

RESULT 96

ID AAK11854 standard; DNA; 507 BP.

DE Human brain expressed single exon probe SEQ ID NO: 11845.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.2%; Score 29; DB 4; Length 507;

Best Local Similarity 100.0%; Pred. No. 0.0026;

RESULT 97

ID AAS41046 standard; cDNA; 923 BP.

DE cDNA encoding novel human enzyme polypeptide #262.

PN WO200155301-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.2%; Score 29; DB 4; Length 923;

Best Local Similarity 100.0%; Pred. No. 0.0027;

RESULT 98

ID AAS41586 standard; cDNA; 981 BP.

DE cDNA encoding novel human enzyme polypeptide #802.

PN WO200155301-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.2%; Score 29; DB 4; Length 981;

Best Local Similarity 100.0%; Pred. No. 0.0027;

RESULT 99

ID AAL01667 standard; cDNA; 981 BP.

DE Human reproductive system related antigen cDNA SEQ ID NO: 1668.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.2%; Score 29; DB 4; Length 981;

Best Local Similarity 100.0%; Pred. No. 0.0027;

RESULT 100

ID AAL05663 standard; DNA; 2751 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8351.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.2%; Score 29; DB 4; Length 2751;

Best Local Similarity 100.0%; Pred. No. 0.0028;

RESULT 101

ID AAD06823 standard; cDNA; 2212 BP.

DE Mouse secreted protein Zalpha37 cDNA.

PN WO200138505-A2.

PD 31-MAY-2001.

PA (ZYMO) ZYMOGENETICS INC.

Query Match 1.1%; Score 26; DB 4; Length 2212;

Best Local Similarity 100.0%; Pred. No. 0.084;

RESULT 102

ID AAC58023 standard; DNA; 24 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:15.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 103

ID AAC58022 standard; DNA; 24 BP.
DE Human PRO1780 forward PCR primer SEQ ID NO:14.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 104

ID AAA37269 standard; DNA; 24 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:284.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 105

ID AAA37268 standard; DNA; 24 BP.
DE Human PRO1780 forward PCR primer SEQ ID NO:283.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 106

ID AAF54403 standard; DNA; 24 BP.
DE DNA encoding protein of the invention #80.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 107

ID AAF54402 standard; DNA; 24 BP.
DE Probe #41 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 108

ID AAD06829 standard; DNA; 24 BP.
DE Human secreted protein Zalpha37 DNA amplifying primer ZC25939.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.

Query Match 1.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 109

ID ACD68441 standard; DNA; 24 BP.
 DE Novel human secreted and transmembrane protein related primer #81.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 110
 ID ACD68442 standard; DNA; 24 BP.
 DE Novel human secreted and transmembrane protein related primer #82.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 111
 ID ACH04544 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 112
 ID ACH04543 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 113
 ID ACD68087 standard; DNA; 24 BP.
 DE Novel human secreted and transmembrane protein related primer #81.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 114
 ID ACD68088 standard; DNA; 24 BP.
 DE Novel human secreted and transmembrane protein related primer #82.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 115
 ID ADC18152 standard; DNA; 24 BP.
 DE Human PRO PCR primer #81.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 116
 ID ADC18153 standard; DNA; 24 BP.

DE Human PRO PCR primer #82.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 117
 ID ADD70798 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 118
 ID ADD70799 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 119
 ID ADD39875 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 120
 ID ADD39876 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 121
 ID ADD70322 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 122
 ID ADD70321 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 123
 ID ADD38442 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.

PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 124
 ID ADD38443 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 125
 ID ADD39399 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 126
 ID ADD39398 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 127
 ID ADD38922 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 128
 ID ADD38921 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 129
 ID ADD40352 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 130
 ID ADD40353 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003082627-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 131
 ID ADE50574 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 132
 ID ADE50573 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 133
 ID ADE20186 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 134
 ID ADE20185 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 135
 ID ADE50096 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 136
 ID ADE50097 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 137
 ID ADE21655 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003082628-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 138
 ID ADE21654 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 139
 ID ADF30080 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 140
 ID ADF30079 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 141
 ID ADF55973 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 142
 ID ADF55972 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 143
 ID ADH99476 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 144
 ID ADH99477 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 145
 ID ADE96657 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 146
 ID ADE96656 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 147
 ID ADF25967 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 148
 ID ADF25968 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 149
 ID ADF24866 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 150
 ID ADF24867 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 RESULT 151
 ID ADF29603 standard; DNA; 24 BP.
 DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 24; DB 12; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 152
ID ADF29602 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 153
ID ADE97134 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 154
ID ADE97133 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 155
ID ADH03172 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 156
ID ADH03171 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 157
ID ADH04125 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 158
ID ADH04126 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 159

ID ADH03649 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 160

ID ADH03648 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 161

ID ADH04603 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 162

ID ADH04602 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 163

ID ADH61604 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 164

ID ADH61603 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 165

ID ADL94803 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 166

ID ADL94802 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 167

ID AAC58051 standard; DNA; 23 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:73.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 168

ID AAF54531 standard; DNA; 23 BP.
DE Primer #137 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 169

ID ACD68570 standard; DNA; 23 BP.
DE Novel human secreted and transmembrane protein related primer #142.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 170

ID ACH04672 standard; DNA; 23 BP.
DE Human secreted/transmembrane protein PRO1780 Taqman PCR primer #2.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 171

ID ACD68216 standard; DNA; 23 BP.
DE Novel human secreted and transmembrane protein related primer #142.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 172

ID ADC18324 standard; DNA; 23 BP.
DE Human PRO PCR primer #139.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 173

ID ADD70970 standard; DNA; 23 BP.

DE Human PRO 1780 Taqman PCR primer #2.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 174
ID ADD40047 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 175
ID ADD70493 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 176
ID ADD38614 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 177
ID ADD39570 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 178
ID ADD39093 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 179
ID ADD40524 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 180
ID ADE50745 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.

PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 181
 ID ADE20357 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 182
 ID ADE50268 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 183
 ID ADE21826 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 184
 ID ADF30251 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 185
 ID ADF56144 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 186
 ID ADH99648 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 187
 ID ADE96828 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003195347-A1.

PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 188
 ID ADF26139 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 189
 ID ADF25038 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 190
 ID ADF29774 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 191
 ID ADE97305 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 192
 ID ADH03343 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 193
 ID ADH04297 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 RESULT 194
 ID ADH03820 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2003224478-A1.
 PD 04-DEC-2003.

PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 195
 ID ADH04774 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 196
 ID ADH61775 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 197
 ID ADL94974 standard; DNA; 23 BP.
 DE Human PRO 1780 Taqman PCR primer #2.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.0%; Score 23; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.2;

RESULT 198
 ID ADQ57767 standard; DNA; 582 BP.
 DE Novel canine microarray-related DNA sequence SeqID9069.
 PN WO2004063324-A2.
 PD 29-JUL-2004.
 PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 1.0%; Score 23; DB 13; Length 582;
 Best Local Similarity 100.0%; Pred. No. 2.5;

RESULT 199
 ID ACN45084 standard; DNA; 49753 BP.
 DE Mouse genomic sequence mCG7831.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.0%; Score 23; DB 11; Length 49753;
 Best Local Similarity 100.0%; Pred. No. 2.8;

RESULT 200
 ID ACH94527 standard; DNA; 582 BP.
 DE Klebsiella pneumoniae polynucleotide seqid 322.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 0.9%; Score 22; DB 11; Length 582;
 Best Local Similarity 100.0%; Pred. No. 7.7;

RESULT 201
 ID ACH94551 standard; DNA; 582 BP.
 DE Klebsiella pneumoniae polynucleotide seqid 346.
 PN US6610836-B1.
 PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 0.9%; Score 22; DB 11; Length 582;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 RESULT 202
 ID ADA19261 standard; cDNA; 1753 BP.
 DE Human insulin resistance marker IRM90 (DJ159A19.3) cDNA.
 PN WO200298355-A2.
 PD 12-DEC-2002.
 PA (CLIN-) CLINGENIX INC.
 Query Match 0.9%; Score 22; DB 10; Length 1753;
 Best Local Similarity 100.0%; Pred. No. 8;
 RESULT 203
 ID ADQ63954 standard; cDNA; 2661 BP.
 DE Novel human cDNA sequence #1115.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 0.9%; Score 22; DB 12; Length 2661;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 RESULT 204
 ID AAD31108 standard; cDNA; 6236 BP.
 DE Human transcription factor and zinc finger protein (TFZN)-8 cDNA.
 PN WO200224895-A2.
 PD 28-MAR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 0.9%; Score 22; DB 6; Length 6236;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 RESULT 205
 ID AAC58050 standard; DNA; 21 BP.
 DE Human PRO1780 hybridisation probe SEQ ID NO:72.
 PN WO200053750-A1.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 0.9%; Score 21; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 22;
 RESULT 206
 ID AAF54530 standard; DNA; 21 BP.
 DE Probe #67 used in the identification of proteins.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 0.9%; Score 21; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 22;
 RESULT 207
 ID ACD68569 standard; DNA; 21 BP.
 DE Novel human secreted and transmembrane protein related probe #63.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.9%; Score 21; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 22;
 RESULT 208
 ID ACH04671 standard; DNA; 21 BP.
 DE Human secreted/transmembrane protein PRO1780 Taqman PCR probe.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 209
ID ACD68215 standard; DNA; 21 BP.
DE Novel human secreted and transmembrane protein related probe #63.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 210
ID ADC18323 standard; DNA; 21 BP.
DE Human PRO probe #68.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 211
ID ADD70969 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 212
ID ADD40046 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 213
ID ADD70492 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 214
ID ADD38613 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 215
ID ADD39569 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 22;
RESULT 216
ID ADD39092 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 217
ID ADD40523 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 218
ID ADE50744 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 219
ID ADE20356 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 220
ID ADE50267 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 221
ID ADE21825 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 222
ID ADF30250 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 223

ID ADF56143 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 224

ID ADH99647 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 225

ID ADE96827 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 226

ID ADF26138 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 227

ID ADF25037 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 228

ID ADF29773 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 229

ID ADE97304 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 230

ID ADH03342 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 231
ID ADH04296 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 232
ID ADH03819 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 233
ID ADH04773 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 234
ID ADH61774 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 235
ID ADL94973 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 236
ID ABA12900 standard; cDNA; 328 BP.
DE Human nervous system related polynucleotide SEQ ID NO 1907.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.9%; Score 20; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 74;
RESULT 237
ID ACF71876 standard; DNA; 369 BP.

DE Photorhabdus luminescens nucleotide sequence #10343.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 0.9%; Score 20; DB 10; Length 369;
 Best Local Similarity 100.0%; Pred. No. 74;
 RESULT 238
 ID ABA18507 standard; DNA; 401 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 10838.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.9%; Score 20; DB 5; Length 401;
 Best Local Similarity 100.0%; Pred. No. 75;
 RESULT 239
 ID ACH33594 standard; cDNA; 465 BP.
 DE Human endothelial cell cDNA #1727.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 0.9%; Score 20; DB 9; Length 465;
 Best Local Similarity 100.0%; Pred. No. 75;
 RESULT 240
 ID ADS50876 standard; cDNA; 654 BP.
 DE Bacterial polynucleotide #5619.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 0.9%; Score 20; DB 13; Length 654;
 Best Local Similarity 100.0%; Pred. No. 76;
 RESULT 241
 ID ABZ80029 standard; cDNA; 3339 BP.
 DE Arabidopsis thaliana phytochrome E encoding cDNA SEQ ID NO:1.
 PN WO2003015500-A2.
 PD 27-FEB-2003.
 PA (PARA-) PARADIGM GENETICS INC.
 Query Match 0.9%; Score 20; DB 10; Length 3339;
 Best Local Similarity 100.0%; Pred. No. 80;
 RESULT 242
 ID ADL27164 standard; DNA; 87761 BP.
 DE Human genomic sequence for hCG23764.
 PN US2003216558-A1.
 PD 20-NOV-2003.
 PA (MORR/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Query Match 0.9%; Score 20; DB 11; Length 87761;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 243

ID ADA03086 standard; DNA; 94529 BP.
 DE Human hCG23764 carcinoma associated gene, SEQ ID NO:1604.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 0.9%; Score 20; DB 9; Length 94529;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 244
 ID ADB72824 standard; DNA; 94529 BP.
 DE Human hCG23764 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 0.9%; Score 20; DB 10; Length 94529;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 245
 ID ADA66370 standard; DNA; 94531 BP.
 DE Human hCG23764 gene genomic DNA sequence.
 PN WO2003053224-A2.
 PD 03-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 0.9%; Score 20; DB 9; Length 94531;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 246
 Query Match 0.9%; Score 20; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 247
 Query Match 0.9%; Score 20; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 248
 Query Match 0.9%; Score 20; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 249
 Query Match 0.9%; Score 20; DB 13; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 89;
 RESULT 250
 ID ADQ97397 standard; DNA; 225587 BP.
 DE Human cancer associated sequence HD08-043, SEQ ID 374.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.9%; Score 20; DB 12; Length 225587;
 Best Local Similarity 100.0%; Pred. No. 91;
 RESULT 251
 ID ADJ11817 standard; DNA; 393 BP.
 DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 453.
 PN US2003135888-A1.
 PD 17-JUL-2003.
 PA (ZHUT/) ZHU T.
 PA (WANG/) WANG X.
 PA (CHAN/) CHANG H.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 0.8%; Score 19; DB 11; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

RESULT 252

ID ADJ11485 standard; DNA; 396 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 121.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 0.8%; Score 19; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

RESULT 253

ID ACH35408 standard; cDNA; 496 BP.
DE Human endothelial cell cDNA #3541.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.

Query Match 0.8%; Score 19; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

RESULT 254

ID AAZ50416 standard; cDNA; 516 BP.
DE Vernonia transcription coactivator PC4(P15) type 1 cDNA.
PN WO200005377-A2.
PD 03-FEB-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.

Query Match 0.8%; Score 19; DB 3; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 255

ID AAL25083 standard; cDNA; 674 BP.
DE Human breast cancer expressed polynucleotide 17540.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 0.8%; Score 19; DB 4; Length 674;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 256

ID AAF44940 standard; cDNA; 719 BP.
DE Human breast cancer related protein coding sequence SEQ ID NO: 96.
PN WO200078960-A2.
PD 28-DEC-2000.

PA (CORI-) CORIXA CORP.

Query Match 0.8%; Score 19; DB 4; Length 719;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 257

ID ACF67756 standard; DNA; 1206 BP.

DE Photorhabdus luminescens nucleotide sequence #6223.

PN WO200294867-A2.

PD 28-NOV-2002.

PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match 0.8%; Score 19; DB 10; Length 1206;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 258

ID ADM91973 standard; DNA; 1212 BP.

DE S pneumoniae antigenic protein-encoding gene sequence SeqID170.

PN WO2004020609-A2.

PD 11-MAR-2004.

PA (TUFT) UNIV TUFTS.

Query Match 0.8%; Score 19; DB 12; Length 1212;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 259

ID ABX07539 standard; DNA; 1218 BP.

DE S. pneumoniae type 4 strain coding region #1827.

PN WO200277021-A2.

PD 03-OCT-2002.

PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

Query Match 0.8%; Score 19; DB 10; Length 1218;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 260

ID ACN43573 standard; cDNA; 1560 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2448.

PN WO2004023973-A2.

PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.

Query Match 0.8%; Score 19; DB 13; Length 1560;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 261

ID ADI43442 standard; DNA; 1563 BP.

DE Plant transcription factor polynucleotide #1304.

PN US2004019927-A1.

PD 29-JAN-2004.

PA (SHER/) SHERMAN B K.

PA (RIEC/) RIECHMANN J L.

PA (JIAN/) JIANG C.

PA (HEAR/) HEARD J E.

PA (HAAK/) HAAKE V.

PA (CREE/) CREELMAN R A.

PA (RATC/) RATCLIFFE O.

PA (ADAM/) ADAM L J.

PA (REUB/) REUBER T L.

PA (KEDD/) KEDDIE J.

PA (BROU/) BROUN P E.

PA (PILG/) PILGRIM M L.

PA (DUBE/) DUBELL A N.

PA (PINE/) PINEDA O.

PA (YUGG/) YU G.

Query Match 0.8%; Score 19; DB 12; Length 1563;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 RESULT 262
 ID ABZ16704 standard; DNA; 1856 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4509.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 0.8%; Score 19; DB 6; Length 1856;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 263
 ID ABZ14955 standard; DNA; 2000 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2760.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 0.8%; Score 19; DB 6; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 264
 ID AAZ52471 standard; DNA; 2206 BP.
 DE HTRM clone 3279329 DNA sequence.
 PN WO9957144-A2.
 PD 11-NOV-1999.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 0.8%; Score 19; DB 3; Length 2206;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 265
 ID ADA13370 standard; cDNA; 2238 BP.
 DE Human intracellular signalling molecule INTSIG-7 cDNA, SEQ ID NO:52.
 PN WO2003031568-A2.
 PD 17-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 0.8%; Score 19; DB 10; Length 2238;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 266
 ID AAH15056 standard; cDNA; 2309 BP.
 DE Human cDNA sequence SEQ ID NO:13052.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 0.8%; Score 19; DB 4; Length 2309;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 267
 ID ADQ18551 standard; DNA; 2309 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1370.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 0.8%; Score 19; DB 12; Length 2309;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 268
 ID ABZ11549 standard; cDNA; 2408 BP.
 DE Human polynucleotide SEQ ID NO 431.
 PN WO200270539-A2.
 PD 12-SEP-2002.

PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 19; DB 6; Length 2408;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 269
 ID ADM44067 standard; cDNA; 2408 BP.
 DE Novel human arginine-rich protein cDNA #431.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Query Match 0.8%; Score 19; DB 12; Length 2408;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 270
 ID ABK49449 standard; cDNA; 2424 BP.
 DE cDNA encoding human transporter protein.
 PN WO200224749-A2.
 PD 28-MAR-2002.
 PA (PEKE) PE CORP NY.
 Query Match 0.8%; Score 19; DB 6; Length 2424;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 271
 ID ABL40302 standard; cDNA; 2628 BP.
 DE Human TLCC-3 cDNA (coding region only).
 PN WO200200718-A2.
 PD 03-JAN-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 0.8%; Score 19; DB 6; Length 2628;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 272
 ID ADQ85330 standard; cDNA; 2678 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2144.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 0.8%; Score 19; DB 12; Length 2678;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 273
 ID AAV07912 standard; DNA; 2699 BP.
 DE Helicobacter pylori 76 kDa polypeptide GHPO 789 DNA.
 PN WO9843479-A1.
 PD 08-OCT-1998.
 PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 19; DB 2; Length 2699;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 274
 ID AAD61566 standard; DNA; 2699 BP.
 DE Helicobacter pylori p76 antigen DNA #2.
 PN US6576244-B1.
 PD 10-JUN-2003.
 PA (ACAM-) ACAMBIS INC.
 Query Match 0.8%; Score 19; DB 10; Length 2699;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 275

ID ABL40301 standard; cDNA; 2724 BP.
DE Human TLCC-3 cDNA.
PN WO200200718-A2.
PD 03-JAN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 0.8%; Score 19; DB 6; Length 2724;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 276

ID AAF22401 standard; cDNA; 2793 BP.
DE Human secreted protein gene 29 SEQ ID NO:39.
PN WO200061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 0.8%; Score 19; DB 3; Length 2793;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 277

ID ABZ73691 standard; cDNA; 2793 BP.
DE Secreted protein-encoding gene 388 cDNA clone HPJBJ51, SEQ ID NO:421.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 8; Length 2793;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 278

ID ABZ67290 standard; cDNA; 2793 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 410.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 10; Length 2793;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 279

ID AAS02554 standard; cDNA; 2795 BP.
DE Human secreted protein gene #35.
PN WO200123409-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 4; Length 2795;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 280

ID ABZ73668 standard; cDNA; 2795 BP.
DE Secreted protein-encoding gene 388 cDNA clone HPJBJ51, SEQ ID NO:398.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 8; Length 2795;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 281

ID ABZ67265 standard; cDNA; 2795 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 385.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 10; Length 2795;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 282

ID AAV72001 standard; DNA; 2798 BP.
 DE Helicobacter pylori 76 kDa polypeptide GHPO 386 DNA.
 PN WO9843479-A1.
 PD 08-OCT-1998.
 PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 19; DB 2; Length 2798;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 283
 ID AAD61565 standard; DNA; 2798 BP.
 DE Helicobacter pylori p76 antigen DNA #1.
 PN US6576244-B1.
 PD 10-JUN-2003.
 PA (ACAM-) ACAMBIS INC.
 Query Match 0.8%; Score 19; DB 10; Length 2798;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 284
 ID ABZ11477 standard; cDNA; 2816 BP.
 DE Human polynucleotide SEQ ID NO 359.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 19; DB 6; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 285
 ID ABZ11958 standard; cDNA; 2816 BP.
 DE Human polynucleotide SEQ ID NO 840.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 19; DB 6; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 286
 ID ABX04986 standard; cDNA; 2816 BP.
 DE Human novel polynucleotide #1.
 PN WO200274961-A1.
 PD 26-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 19; DB 8; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 287
 ID ADM44476 standard; cDNA; 2816 BP.
 DE Novel human arginine-rich protein cDNA #840.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Query Match 0.8%; Score 19; DB 12; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 288
 ID ADM43995 standard; cDNA; 2816 BP.
 DE Novel human arginine-rich protein cDNA #359.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.

PA (DRMA/) DRMANAC R T.
 Query Match 0.8%; Score 19; DB 12; Length 2816;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 289
 ID ADQ63624 standard; cDNA; 2954 BP.
 DE Novel human cDNA sequence #785.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 0.8%; Score 19; DB 12; Length 2954;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 290
 ID AAV44295 standard; cDNA; 3550 BP.
 DE Human secreted protein clone CJ145_1 cDNA.
 PN WO9827205-A2.
 PD 25-JUN-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 0.8%; Score 19; DB 2; Length 3550;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 291
 ID AAF98469 standard; cDNA; 3550 BP.
 DE Human cDNA clone CJ145_1 sequence SEQ ID 160.
 PN WO200119988-A1.
 PD 22-MAR-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 0.8%; Score 19; DB 5; Length 3550;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 292
 ID ADQ23023 standard; DNA; 4046 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 0.8%; Score 19; DB 12; Length 4046;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 293
 ID ACN40547 standard; cDNA; 4282 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA326649, SEQ ID NO:5391.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 19; DB 13; Length 4282;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 294
 ID AAI58667 standard; cDNA; 4352 BP.
 DE Human polynucleotide SEQ ID NO 870.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 19; DB 4; Length 4352;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 295
 ID ADQ98885 standard; cDNA; 4352 BP.
 DE DNA encoding human GPCR-like protein seqid 555.
 PN US6569662-B1.
 PD 27-MAY-2003.
 PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 19; DB 5; Length 4352;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 296

ID ADB48645 standard; cDNA; 4352 BP.
DE Novel human cDNA SEQ ID NO 555.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.

Query Match 0.8%; Score 19; DB 9; Length 4352;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 297

ID AAI60453 standard; cDNA; 4377 BP.
DE Human polynucleotide SEQ ID NO 4442.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 19; DB 4; Length 4377;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 298

ID ACN45184 standard; DNA; 26533 BP.
DE Mouse genomic sequence mCG9336.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 0.8%; Score 19; DB 11; Length 26533;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 299

ID AAV52204 standard; DNA; 32768 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:71.
PN WO9818931-A2.,
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 19; DB 2; Length 32768;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 300

ID ACN44896 standard; DNA; 40568 BP.
DE Mouse genomic sequence mCG54271.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 0.8%; Score 19; DB 11; Length 40568;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 301

ID AAX23518 standard; DNA; 49998 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 2.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.

Query Match 0.8%; Score 19; DB 2; Length 49998;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 302

ID ABD33295 standard; DNA; 64125 BP..
DE Human cancer-associated (CA) gene HD07-052.

PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 13; Length 64125;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 RESULT 303
 ID ACN44320 standard; DNA; 77941 BP.
 DE Mouse genomic sequence mCG17383.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 0.8%; Score 19; DB 11; Length 77941;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 304
 ID ACN37242 standard; DNA; 78294 BP.
 DE Human periodontal disease related gene PTGER3 SEQ ID NO:152.
 Query Match 0.8%; Score 19; DB 13; Length 78294;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 305
 ID ADQ59189 standard; DNA; 81679 BP.
 DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:26.
 PN KR2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G.
 PA (KIMN/) KIM N G.
 PA (LEEJ/) LEE J S.
 PA (RHEE/) RHEE H S.
 Query Match 0.8%; Score 19; DB 12; Length 81679;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 306
 ID ADQ97298 standard; DNA; 95484 BP.
 DE Mouse cancer associated sequence MD08-028, SEQ ID 275.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 12; Length 95484;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 307
 Query Match 0.8%; Score 19; DB 2; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 308
 Query Match 0.8%; Score 19; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 309
 Query Match 0.8%; Score 19; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 310
 Query Match 0.8%; Score 19; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 311
 Query Match 0.8%; Score 19; DB 10; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 312
 ID ABD32921 standard; DNA; 754086 BP.
 DE Mouse cancer-associated genomic DNA MD19-002.
 PN WO2004074320-A2.
 PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 13; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 313
 ID ABD32923 standard; DNA; 788759 BP.
 DE Human cancer-associated genomic DNA HD19-002.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 13; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 314
 ID AAX20249 standard; DNA; 116277 BP.
 DE Borrelia burgdorferi polynucleotide sequence #2.
 PN WO9858943-A1.
 PD 30-DEC-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (MEDI-) MEDIMMUNE INC.
 Query Match 0.8%; Score 19; DB 2; Length 116277;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 315
 ID ADQ97301 standard; DNA; 127722 BP.
 DE Human cancer associated sequence HD08-028, SEQ ID 278.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 12; Length 127722;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 316
 ID ADQ97651 standard; DNA; 127943 BP.
 DE Human cancer associated sequence HD10-021, SEQ ID 628.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 0.8%; Score 19; DB 12; Length 127943;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 317
 ID ABK49450 standard; DNA; 147309 BP.
 DE Human transporter genomic DNA sequence.
 Query Match 0.8%; Score 19; DB 6; Length 147309;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 318
 ID ADR52892 standard; DNA; 151152 BP.
 DE Drug therapy altered expressed gene #243.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC/) BURCZYNSKI M.
 PA (TWIN/) TWINE N.
 PA (DORN/) DORNER A J.
 PA (TREP/) TREPICCHIO W L.
 Query Match 0.8%; Score 19; DB 13; Length 151152;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 319
 ID ACF62730 standard; DNA; 164702 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.
 PN WO2003013534-A2.

PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 0.8%; Score 19; DB 8; Length 164702;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 320
 ID ADB20845 standard; DNA; 164702 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:658.
 PN WO2003013533-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 0.8%; Score 19; DB 8; Length 164702;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 321
 ID ADB87934 standard; DNA; 164702 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:658.
 PN WO2003013536-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 0.8%; Score 19; DB 10; Length 164702;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 322
 ID ADB96917 standard; DNA; 164702 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:658.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 0.8%; Score 19; DB 10; Length 164702;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 323
 ID ADB92108 standard; DNA; 164702 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:658.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 0.8%; Score 19; DB 10; Length 164702;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 324
 ID AAD58431 standard; DNA; 322101 BP.
 DE Human PAOD1 genomic DNA.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 0.8%; Score 19; DB 10; Length 322101;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 RESULT 325
 ID ADI35046 standard; DNA; 322101 BP.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) genomic DNA sequence.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 0.8%; Score 19; DB 12; Length 322101;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 RESULT 326
 ID AAC58049 standard; DNA; 18 BP.
 DE Human PRO1780 forward PCR primer SEQ ID NO:71.
 PN WO200053750-A1.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 327
 ID AAF54529 standard; DNA; 18 BP.
 DE Primer #136 used in the identification of proteins.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 328
 ID ACD68568 standard; DNA; 18 BP.
 DE Novel human secreted and transmembrane protein related primer #141.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 329
 ID ACH04670 standard; DNA; 18 BP.
 DE Human secreted/transmembrane protein PRO1780 Taqman PCR primer #1.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 330
 ID ACD68214 standard; DNA; 18 BP.
 DE Novel human secreted and transmembrane protein related primer #141.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 331
 ID ADC18322 standard; DNA; 18 BP.
 DE Human PRO PCR primer #138.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 332
 ID ADD70968 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 333
 ID ADD40045 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 334
 ID ADD70491 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 335
 ID ADD38612 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 336
 ID ADD39568 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 337
 ID ADD39091 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 338
 ID ADD40522 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 339
 ID ADE50743 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 340
 ID ADE20355 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 341
 ID ADE50266 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 342
 ID ADE21824 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 343
 ID ADF30249 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 344
 ID ADF56142 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 345
 ID ADH99646 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 346
 ID ADE96826 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 347
 ID ADF26137 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 348

ID ADF25036 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 349

ID ADF29772 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 350

ID ADE97303 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 351

ID ADH03341 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 352

ID ADH04295 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 353

ID ADH03818 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 354

ID ADH04772 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 355

ID ADH61773 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 356
 ID ADL94972 standard; DNA; 18 BP.
 DE Human PRO 1780 Taqman PCR primer #1.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 RESULT 357
 ID AAA96250 standard; DNA; 31 BP.
 DE PCR primer for cDNA encoding a human Edg5 polypeptide.
 PN WO200056135-A2.
 PD 28-SEP-2000.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 0.8%; Score 18; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 RESULT 358
 ID ADF99932 standard; cDNA; 90 BP.
 DE Nicotiana tabacum variant bright yellow nucleotide sequence SEQ ID:448.
 PN WO2003097790-A2.
 PD 27-NOV-2003.
 PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA (VTTB-) VTT BIOTECHNOLOGY.
 Query Match 0.8%; Score 18; DB 12; Length 90;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 RESULT 359
 ID ACD70068 standard; DNA; 100 BP.
 DE E. coli K12 MG1655 biochip probe SEQ ID 1338.
 PN EP1260592-A1.
 PD 27-NOV-2002.
 PA (MWGB-) MWG-BIOTECH AG.
 Query Match 0.8%; Score 18; DB 8; Length 100;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 RESULT 360
 ID ACD70069 standard; DNA; 100 BP.
 DE E. coli K12 MG1655 biochip probe SEQ ID 1339.
 PN EP1260592-A1.
 PD 27-NOV-2002.
 PA (MWGB-) MWG-BIOTECH AG.
 Query Match 0.8%; Score 18; DB 8; Length 100;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 RESULT 361
 ID ADO13357 standard; DNA; 113 BP.
 DE SNP target #221 for single multiplex PCR detection method.
 PN WO2004033649-A2.
 PD 22-APR-2004.
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 Query Match 0.8%; Score 18; DB 12; Length 113;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 RESULT 362

ID AAF17410 standard; DNA; 220 BP.
 DE K-DNA cleavage hotspot.
 PN US6150160-A.
 PD 21-NOV-2000.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYPE-) UNIV PENNSYLVANIA.
 Query Match 0.8%; Score 18; DB 4; Length 220;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 363
 ID ADF12345 standard; DNA; 220 BP.
 DE Human retrotransposon L1 EN substrate K-DNA.
 PN US2003121063-A1.
 PD 26-JUN-2003.
 PA (UYPE-) UNIV PENNSYLVANIA.
 Query Match 0.8%; Score 18; DB 10; Length 220;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 364
 ID ADF58236 standard; cDNA; 240 BP.
 DE Human polynucleotide sequence SEQ ID NO:603.
 PN WO2003080795-A2.
 PD 02-OCT-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 18; DB 10; Length 240;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 365
 ID ADL85483 standard; DNA; 245 BP.
 DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1876.
 PN WO2003093445-A2.
 PD 13-NOV-2003.
 PA (STOW-) STOWERS INST MEDICAL RES.
 Query Match 0.8%; Score 18; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 366
 ID ADL85482 standard; DNA; 245 BP.
 DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1875.
 PN WO2003093445-A2.
 PD 13-NOV-2003.
 PA (STOW-) STOWERS INST MEDICAL RES.
 Query Match 0.8%; Score 18; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 367
 ID ACH88858 standard; DNA; 287 BP.
 DE Human genome derived single exon probe #22053.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 0.8%; Score 18; DB 12; Length 287;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 368
 ID ADT96283 standard; cDNA; 295 BP.
 DE Colon cancer associated human cDNA sequence #1790.
 PN US2003087818-A1.
 PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 0.8%; Score 18; DB 11; Length 295;

Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 369
 ID AAZ32844 standard; DNA; 303 BP.
 DE Human chemokine beta-R1 promoter.
 PN US5977334-A.
 PD 02-NOV-1999.
 PA (CLEV-) CLEVELAND CLINIC FOUND.
 Query Match 0.8%; Score 18; DB 3; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 370
 ID ABN84846 standard; DNA; 303 BP.
 DE Human Beta R1 chemokine gene promoter.
 PN US6414118-B1.
 PD 02-JUL-2002.
 PA (CLEV-) CLEVELAND CLINIC FOUND.
 Query Match 0.8%; Score 18; DB 6; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 RESULT 371
 ID AAS34210 standard; cDNA; 350 BP.
 DE Human cDNA encoding a novel foetal antigen, SEQ ID No 734.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 5; Length 350;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 372
 ID ABQ85759 standard; DNA; 355 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 629.
 PN US2002062014-A1.
 PD 23-MAY-2002.
 PA (GORL/) GORLACH J.
 PA (ANYY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYU/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match 0.8%; Score 18; DB 6; Length 355;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 373
 ID AAV87586 standard; cDNA; 361 BP.
 DE EST clone DY656.
 PN WO9845437-A2.
 PD 15-OCT-1998.
 PA (GEMY) GENETICS INST INC.

Query Match 0.8%; Score 18; DB 2; Length 361;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 374
 ID AAA44800 standard; cDNA; 365 BP.
 DE Human secreted expressed sequence tag SEQ ID NO:1375.
 PN WO200021991-A1.
 PD 20-APR-2000.
 PA (GEMY) GENETICS INST INC.
 Query Match 0.8%; Score 18; DB 3; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 375
 ID ADP66197 standard; cDNA; 365 BP.
 DE Human cDNA from gene modulated by pro-inflammatory cytokines #17.
 PN US2004110194-A1.
 PD 10-JUN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 0.8%; Score 18; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 376
 ID ABL79277 standard; cDNA; 399 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:2255.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 0.8%; Score 18; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 377
 ID AAD15302 standard; cDNA; 402 BP.
 DE Human PMS134 cDNA.
 PN WO200161012-A1.
 PD 23-AUG-2001.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 PA (KINZ/) KINZLER K.
 PA (VOGE/) VOGELSTEIN B.
 Query Match 0.8%; Score 18; DB 4; Length 402;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 378
 ID ACH46946 standard; cDNA; 402 BP.
 DE Human infant brain cDNA #1009.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 0.8%; Score 18; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 379
 ID AAH76368 standard; cDNA; 426 BP.
 DE Human PMS2-134 cDNA.
 PN WO200159092-A2.
 PD 16-AUG-2001.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 0.8%; Score 18; DB 4; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 380
 ID AAH75045 standard; cDNA; 426 BP.
 DE Nucleotide sequence of human mismatch repair protein PMS2-134.
 PN WO200162945-A1.
 PD 30-AUG-2001.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (NICO/) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 PA (GRAS/) GRASSO L.
 PA (VOGE/) VOGELSTEIN B.
 PA (KINZ/) KINZLER K W.
 Query Match 0.8%; Score 18; DB 5; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 381
 ID ABK86092 standard; DNA; 426 BP.
 DE Human cDNA encoding PMS2-134.
 PN WO200238750-A1.
 PD 16-MAY-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 382
 ID AAD39201 standard; cDNA; 426 BP.
 DE Human mismatch repair protein, hPMS2-134 cDNA.
 PN WO200237967-A1.
 PD 16-MAY-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 383
 ID AAL48701 standard; DNA; 426 BP.
 DE Human truncated mismatch repair protein PMS2-134 coding sequence.
 PN WO200254856-A1.
 PD 18-JUL-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 384
 ID AAD39773 standard; cDNA; 426 BP.
 DE Human PMS2-134 cDNA.
 PN WO200240499-A1.
 PD 23-MAY-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 385
 ID ABX12943 standard; DNA; 426 BP.
 DE DNA encoding human PMS2-134 protein.
 PN WO2003012130-A1.
 PD 13-FEB-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 8; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 RESULT 386
 ID ACA89707 standard; cDNA; 426 BP.
 DE cDNA encoding human PMS2-134 mismatch repair protein.

PN WO2003031937-A2.

PD 17-APR-2003.

PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 8; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 387

ID AAL57767 standard; cDNA; 426 BP.

DE Human mismatch repair protein PMS2-134 cDNA.

PN WO2003062435-A1.

PD 31-JUL-2003.

PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 9; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 388

ID ADA06251 standard; DNA; 426 BP.

DE DNA encoding the human mismatch repair, MMR, protein PMS2-134.

PN US2003068808-A1.

PD 10-APR-2003.

PA (NICO/) NICOLAIDES N C.

PA (SASS/) SASS P M.

PA (GRAS/) GRASSO L.

PA (KLIN/) KLINE J B.

Query Match 0.8%; Score 18; DB 9; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 389

ID ADC89614 standard; cDNA; 426 BP.

DE Human PMS2-134 encoding cDNA SEQ ID NO:14.

PN WO2003072732-A2.

PD 04-SEP-2003.

PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 10; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 390

ID ADF17899 standard; DNA; 426 BP.

DE Human PMS2-134 cDNA, a mismatch repair gene.

PN US6576468-B1.

PD 10-JUN-2003.

PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 10; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 391

ID ADG62906 standard; cDNA; 426 BP.

DE Human dominant negative mismatch repair protein (PMS2-134) cDNA.

PN US2003165468-A1.

PD 04-SEP-2003.

PA (GRAS/) GRASSO L.

PA (NICO/) NICOLAIDES N C.

PA (SASS/) SASS P M.

Query Match 0.8%; Score 18; DB 10; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 392

ID ADH62636 standard; cDNA; 426 BP.

DE Human mismatch repair protein PMS2-134 cDNA.

PN US2003143682-A1.

PD 31-JUL-2003.

PA (NICO/) NICOLAIDES N C.

PA (GRAS/) GRASSO L.

PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 10; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 393
 ID ADF78847 standard; cDNA; 426 BP.
 DE Human dominant negative truncation hPMS2-134.
 PN US2003186441-A1.
 PD 02-OCT-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 12; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 394
 ID ADG46774 standard; cDNA; 426 BP.
 DE Human MMR protein (mismatch protein), PMS2-134 cDNA.
 PN US2003091997-A1.
 PD 15-MAY-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 12; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 395
 ID ADO40073 standard; cDNA; 426 BP.
 DE Human PMS2-134 mutant cDNA.
 PN US6737268-B1.
 PD 18-MAY-2004.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 12; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 396
 ID ADP66683 standard; DNA; 426 BP.
 DE Human mismatch repair protein PMS2-134 encoding DNA.
 PN WO2004046330-A2.
 PD 03-JUN-2004.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 12; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 397
 ID ADR13890 standard; cDNA; 426 BP.
 DE Human DNA mismatch repair protein PMS2-134 cDNA.
 PN US2004158886-A1.
 PD 12-AUG-2004.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 13; Length 426;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 398
 ID ACA43798 standard; DNA; 462 BP.
 DE Prokaryotic essential gene #25455.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 0.8%; Score 18; DB 8; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 399
 ID ADR29948 standard; cDNA; 475 BP.

DE Mouse gene trapped cDNA sequence, GTS #525.
PN US2004168209-A1.
PD 26-AUG-2004.
PA (ABUI/) ABUIN A.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.

Query Match 0.8%; Score 18; DB 13; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 400

ID ACH50718 standard; cDNA; 501 BP.
DE Human mammary gland cDNA #123.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.

Query Match 0.8%; Score 18; DB 9; Length 501;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 401

ID ACH75158 standard; DNA; 507 BP.
DE Human genome derived single exon probe #8353.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match 0.8%; Score 18; DB 12; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 402

ID ADQ79683 standard; DNA; 507 BP.
DE Benzoate dioxygenase beta subunit (benB) DNA.
PN KR2003082683-A.
PD 23-OCT-2003.
PA (KIME/) KIM E S.

Query Match 0.8%; Score 18; DB 12; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 403

ID AAH11550 standard; cDNA; 541 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:8385.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.

Query Match 0.8%; Score 18; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 404

ID ABV52391 standard; cDNA; 547 BP.
DE Human prostate expression marker cDNA 52382.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 0.8%; Score 18; DB 5; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 405

ID ADQ56077 standard; DNA; 554 BP.
DE Novel canine microarray-related DNA sequence SeqID7379.

PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.

Query Match 0.8%; Score 18; DB 13; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 406

ID ABX78375 standard; cDNA; 585 BP.
DE Rice stress response protein EST #8.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.

Query Match 0.8%; Score 18; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 407

ID AAC10739 standard; cDNA; 587 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14814.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.

Query Match 0.8%; Score 18; DB 3; Length 587;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 408

ID ABV55372 standard; cDNA; 590 BP.
DE Human prostate expression marker cDNA 55363.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 0.8%; Score 18; DB 5; Length 590;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 409

ID ADQ51591 standard; DNA; 609 BP.
DE Novel canine microarray-related DNA sequence SeqID2893.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.

Query Match 0.8%; Score 18; DB 13; Length 609;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 410

ID AAA65944 standard; DNA; 636 BP.
DE E. coli proliferation associated coding sequence SEQ ID NO:136.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.

Query Match 0.8%; Score 18; DB 3; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;

RESULT 411

ID ABV55471 standard; cDNA; 637 BP.

DE Human prostate expression marker cDNA 55462.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 0.8%; Score 18; DB 5; Length 637;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 412
 ID AAT29625 standard; cDNA to mRNA; 649 BP.
 DE DNA mismatch repair protein coding sequence fragment PMS 5.
 PN JP08107797-A.
 PD 30-APR-1996.
 PA (GANK-) ZH GAN KENKYUKAI.
 PA (EISA) EISAI CO LTD.
 Query Match 0.8%; Score 18; DB 2; Length 649;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 413
 ID ABL67265 standard; DNA; 649 BP.
 DE Thyroid cancer related gene sequence SEQ ID NO:5602.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 0.8%; Score 18; DB 6; Length 649;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 414
 ID ACN92881 standard; DNA; 711 BP.
 DE Breast cancer related marker, seq id 14031.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 0.8%; Score 18; DB 11; Length 711;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 415
 ID ADK16796 standard; DNA; 738 BP.
 DE Nanoarchaeum equitans cancer-associated (CA) gene #374.
 PN WO2003093434-A2.
 PD 13-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 0.8%; Score 18; DB 12; Length 738;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 416
 ID ADT48090 standard; cDNA; 750 BP.
 DE Bacterial polynucleotide #22841.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 0.8%; Score 18; DB 13; Length 750;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 RESULT 417
 ID ACA27682 standard; DNA; 765 BP.
 DE Prokaryotic essential gene #9339.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.

Query Match 0.8%; Score 18; DB 8; Length 765;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 418
 ID ADE07742 standard; DNA; 777 BP.
 DE Novel coding sequence (useful for identifying genetic disorders) #808.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 18; DB 10; Length 777;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 419
 ID AAS63236 standard; cDNA; 780 BP.
 DE Escherichia coli endonuclease III (Endo III) nth gene.
 PN WO200173079-A2.
 PD 04-OCT-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 0.8%; Score 18; DB 4; Length 780;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 420
 ID ADE07014 standard; DNA; 828 BP.
 DE Novel coding sequence (useful for identifying genetic disorders) #80.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 18; DB 10; Length 828;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 421
 ID AAK93666 standard; cDNA; 849 BP.
 DE Human cDNA clone representative sequence, SEQ ID NO: 2126.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 0.8%; Score 18; DB 4; Length 849;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 422
 ID AAK92006 standard; cDNA; 849 BP.
 DE Human cDNA 5'-end sequence, SEQ ID NO: 466.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 0.8%; Score 18; DB 4; Length 849;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 423
 ID ADL28433 standard; cDNA; 849 BP.
 DE 5' end of a human cDNA molecule SeqID 466.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 0.8%; Score 18; DB 12; Length 849;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 424
 ID ADL30093 standard; cDNA; 849 BP.
 DE 3' end of a representative human cDNA cluster SeqID 2126.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 0.8%; Score 18; DB 12; Length 849;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 425
 ID AAS02360 standard; DNA; 870 BP.
 DE Neomycin phosphotransferase gene.
 PN WO200123541-A2.
 PD 05-APR-2001.
 PA (ALEX-) ALEXION PHARM INC.
 Query Match 0.8%; Score 18; DB 4; Length 870;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 426
 ID AAS02357 standard; DNA; 872 BP.
 DE Promoterless neomycin phosphotransferase gene cassette.
 PN WO200123541-A2.
 PD 05-APR-2001.
 PA (ALEX-) ALEXION PHARM INC.
 Query Match 0.8%; Score 18; DB 4; Length 872;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 427
 ID ADP79709 standard; DNA; 1023 BP.
 DE Cycloclasticus aromatic ring dioxygenase gene cluster gene #4.
 PN WO2004050875-A1.
 PD 17-JUN-2004.
 PA (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
 Query Match 0.8%; Score 18; DB 13; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 RESULT 428
 ID AAK87321 standard; DNA; 1283 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42133.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 4; Length 1283;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 429
 ID ADT41893 standard; cDNA; 1284 BP.
 DE Bacterial polynucleotide #16644.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 0.8%; Score 18; DB 13; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 430
 ID ACC60654 standard; DNA; 1302 BP.
 DE Gene sequence #SEQ ID 90.
 PN EP1258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.
 Query Match 0.8%; Score 18; DB 10; Length 1302;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 431
 ID ADK64151 standard; DNA; 1302 BP.
 DE Disease treating protein complex-derived gene #1300.
 PN EP1338608-A2.

PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 0.8%; Score 18; DB 10; Length 1302;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 432
ID AAC53146 standard; DNA; 1331 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 73531.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 18; DB 3; Length 1331;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 433
ID AAS34787 standard; cDNA; 1422 BP.
DE cDNA encoding novel human neoplastic disease associated polypeptide #21.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 4; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 434
ID ABK43162 standard; cDNA; 1422 BP.
DE cDNA encoding human DNA repair and processing protein, SEQ ID No 22.
PN WO200155305-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 4; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 435
ID ADC45945 standard; cDNA; 1422 BP.
DE Human neoplastic disease-associated gene 21 cDNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 10; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 436
ID ADA68340 standard; DNA; 1443 BP.
DE Arabidopsis thaliana gene, SEQ ID 792.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 0.8%; Score 18; DB 8; Length 1443;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 437
ID ABQ73708 standard; cDNA; 1455 BP.
DE Human colon specific nucleic acid (CSNA) SEQ ID NO:14.
PN WO200248370-A2..
PD 20-JUN-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 0.8%; Score 18; DB 6; Length 1455;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 438
ID AAN30040 standard; DNA; 1480 BP.
DE Sequence encoding bovine leukocyte interferon (IFN) -alpha-2 on plasmid
DE subclone p678EcoRI 3.2 kb.
PN EP88622-A.
PD 14-SEP-1983.

PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 1; Length 1480;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 439

ID AAV08178 standard; DNA; 1480 BP.

DE Bovine interferon-alpha 2 DNA.

PN US5827694-A.

PD 27-OCT-1998.

PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 2; Length 1480;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 440

ID AAV68161 standard; DNA; 1480 BP.

DE Bovine interferon-alpha 2 DNA.

PN US5831023-A.

PD 03-NOV-1998.

PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 2; Length 1480;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 441

ID ABS53994 standard; cDNA; 1480 BP.

DE cDNA encoding bovine leukocyte interferon alpha 2 (BoIFN-alpha2).

PN US6432677-B1.

PD 13-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match 0.8%; Score 18; DB 6; Length 1480;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 442

ID AAS85584 standard; cDNA; 1488 BP.

DE DNA encoding novel human diagnostic protein #21388.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 5; Length 1488;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 443

ID AAH67065 standard; DNA; 1494 BP.

DE C glutamicum coding sequence fragment SEQ ID NO: 2100.

PN EP1108790-A2.

PD 20-JUN-2001.

PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 0.8%; Score 18; DB 5; Length 1494;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 444

ID ADK65960 standard; DNA; 1497 BP.

DE C glutamicum mutated sigA gene #1.

PN DE10162729-A1.

PD 03-JUL-2003.

PA (DEGS) DEGUSSA AG.

Query Match 0.8%; Score 18; DB 10; Length 1497;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 445

ID ADK65958 standard; DNA; 1497 BP.

DE C glutamicum wild-type sigA gene.

PN DE10162729-A1.

PD 03-JUL-2003.

PA (DEGS) DEGUSSA AG.

Query Match 0.8%; Score 18; DB 10; Length 1497;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 446
 ID ABV24039 standard; cDNA; 1503 BP.
 DE Human prostate expression marker cDNA 24030.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 0.8%; Score 18; DB 5; Length 1503;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 447
 ID ABV29922 standard; cDNA; 1504 BP.
 DE Human prostate expression marker cDNA 29913.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 0.8%; Score 18; DB 5; Length 1504;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 448
 ID AAD45435 standard; cDNA; 1565 BP.
 DE Human MLH3 mutant cDNA #2.
 PN US6416984-B1.
 PD 09-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 6; Length 1565;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 449
 ID ADC91963 standard; DNA; 1602 BP.
 DE E. faecium DNA sequence SEQ ID 1590.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 0.8%; Score 18; DB 10; Length 1602;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 450
 ID ADQ23147 standard; DNA; 1623 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5967.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 0.8%; Score 18; DB 12; Length 1623;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 451
 ID ADD13289 standard; DNA; 1624 BP.
 DE C. glutamicum stability and folding associated DNA RXA03793.
 PN WO2003040180-A2.
 PD 15-MAY-2003.
 PA (BADI) BASF AG.
 Query Match 0.8%; Score 18; DB 10; Length 1624;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 RESULT 452
 ID AAI99791 standard; cDNA; 1626 BP.
 DE Human eukaryotic acetyl transferase 10 encoding cDNA.
 PN WO200175026-A2.
 PD 11-OCT-2001.
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 Query Match 0.8%; Score 18; DB 6; Length 1626;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 453

ID ADQ25162 standard; DNA; 1634 BP.

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7982.

PN WO2004048938-A2.

PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 0.8%; Score 18; DB 12; Length 1634;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 454

ID AAV34296 standard; DNA; 1688 BP.

DE Human secreted protein gene 11 clone HLTBS22.

PN WO9840483-A2.

PD 17-SEP-1998.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 18; DB 2; Length 1688;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 455

ID AAD44646 standard; cDNA; 1688 BP.

DE Human secreted protein-encoding gene 11 cDNA clone HLTBS22, SEQ ID NO:21.

PN US2002077287-A1.

PD 20-JUN-2002.

PA (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

Query Match 0.8%; Score 18; DB 6; Length 1688;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 456

ID AAD44864 standard; cDNA; 1688 BP.

DE Human secreted protein-encoding gene 11 cDNA clone HLTBS22, SEQ ID NO:21.

PN US2002076756-A1.

PD 20-JUN-2002.

PA (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

Query Match 0.8%; Score 18; DB 6; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 457

ID ABX96976 standard; cDNA; 1688 BP.
DE Human secreted protein gene 11, cDNA.
PN US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.

Query Match 0.8%; Score 18; DB 8; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 458

ID ADG89748 standard; cDNA; 1688 BP.
DE Human cDNA from secreted protein gene 11.
PN US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

Query Match 0.8%; Score 18; DB 12; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 459

ID ABZ24411 standard; cDNA; 1692 BP.
DE Human TBC1D1 nucleic acid 18558614.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 0.8%; Score 18; DB 8; Length 1692;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 460

ID AAF15885 standard; cDNA; 1756 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:320.
PN WO200055174-A1.

PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 Query Match 0.8%; Score 18; DB 3; Length 1756;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 461
 ID ACN39313 standard; cDNA; 1764 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325551, SEQ ID NO:3378.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 0.8%; Score 18; DB 13; Length 1764;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 462
 ID AAC46205 standard; DNA; 1767 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49283.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 0.8%; Score 18; DB 3; Length 1767;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 463
 ID AAH76370 standard; cDNA; 1785 BP.
 DE Human PMSR3 cDNA.
 PN WO200159092-A2.
 PD 16-AUG-2001.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 0.8%; Score 18; DB 4; Length 1785;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 464
 ID AAH75047 standard; cDNA; 1785 BP.
 DE Nucleotide sequence of human mismatch repair protein PMSR3.
 PN WO200162945-A1.
 PD 30-AUG-2001.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (NICO/) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 PA (GRAS/) GRASSO L.
 PA (VOGE/) VOGELSTEIN B.
 PA (KINZ/) KINZLER K W.
 Query Match 0.8%; Score 18; DB 5; Length 1785;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 465
 ID ABX12946 standard; DNA; 1785 BP.
 DE DNA encoding human PMSR3 protein.
 PN WO2003012130-A1.
 PD 13-FEB-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 8; Length 1785;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 466
 ID ACA89710 standard; cDNA; 1785 BP.
 DE cDNA encoding human PMSR3 mismatch repair protein.
 PN WO2003031937-A2.
 PD 17-APR-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 8; Length 1785;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 467

ID AAL57773 standard; cDNA; 1785 BP.
DE Human mismatch repair protein PMSR3 cDNA.
PN WO2003062435-A1..
PD 31-JUL-2003.
PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 9; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 468

ID ADA06257 standard; DNA; 1785 BP.
DE DNA encoding the human mismatch repair, MMR, protein PMSR3.
PN US2003068808-A1.
PD 10-APR-2003.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (KLIN/) KLINE J B.

Query Match 0.8%; Score 18; DB 9; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 469

ID ADG62897 standard; cDNA; 1785 BP.
DE Human PMSR3 cDNA.
PN US2003165468-A1.
PD 04-SEP-2003.
PA (GRAS/) GRASSO L.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.

Query Match 0.8%; Score 18; DB 10; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 470

ID ADP66687 standard; DNA; 1785 BP.
DE Human mismatch repair protein PMSR3 encoding DNA.
PN WO2004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 12; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 471

ID AAV04064 standard; cDNA; 1817 BP.
DE Human RNA-binding protein ZPR1 cDNA.
PN WO9746684-A1.
PD 11-DEC-1997.
PA (UYMA-) UNIV MASSACHUSETTS.

Query Match 0.8%; Score 18; DB 2; Length 1817;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 472

ID ADR25106 standard; DNA; 1817 BP.
DE Breast cancer prognosis marker #967.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.

Query Match 0.8%; Score 18; DB 13; Length 1817;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 473

ID ADT44238 standard; cDNA; 1826 BP.
DE Bacterial polynucleotide #18989.

PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 0.8%; Score 18; DB 13; Length 1826;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 474
 ID ADQ79682 standard; DNA; 1853 BP.
 DE Benzoate catabolic enzyme gene cluster #2.
 PN KR2003082683-A.
 PD 23-OCT-2003.
 PA (KIME/) KIM E S.
 Query Match 0.8%; Score 18; DB 12; Length 1853;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 475
 ID ABX78376 standard; cDNA; 1861 BP.
 DE Rice stress response protein EST #9.
 PN US2002152497-A1.
 PD 17-OCT-2002.
 PA (FALC/) FALCO S C.
 PA (FAMO/) FAMODU O O.
 PA (MEYE/) MEYERS B C.
 PA (MIAO/) MIAO G.
 PA (ODEL/) ODELL J T.
 PA (RAFA/) RAFALSKI J A.
 PA (THOR/) THORPE C J.
 PA (SAKA/) SAKAI H.
 PA (WENG/) WENG Z.
 Query Match 0.8%; Score 18; DB 10; Length 1861;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 476
 ID ADK65962 standard; DNA; 1892 BP.
 DE C glutamicum mutated sigA gene #2.
 PN DE10162729-A1.
 PD 03-JUL-2003.
 PA (DEGS) DEGUSSA AG.
 Query Match 0.8%; Score 18; DB 10; Length 1892;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 477
 ID AAS75603 standard; cDNA; 1911 BP.
 DE DNA encoding novel human diagnostic protein #11407.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 18; DB 5; Length 1911;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 RESULT 478
 ID ABK40202 standard; cDNA; 1920 BP.
 DE Human G protein-coupled receptor (GPCR) 8 cDNA.
 PN WO200202637-A2.
 PD 10-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 0.8%; Score 18; DB 6; Length 1920;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 479

ID ADS59106 standard; cDNA; 1935 BP.
DE Bacterial polynucleotide #11093.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 0.8%; Score 18; DB 13; Length 1935;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 480

ID ABQ72684 standard; cDNA; 1980 BP.
DE Human MDDT encoding cDNA SEQ ID NO 236.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 6; Length 1980;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 481

ID ABL90639 standard; cDNA; 1997 BP.
DE Human polynucleotide SEQ ID NO 1201.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 18; DB 6; Length 1997;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 482

ID ACC61223 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 1228.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.

Query Match 0.8%; Score 18; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 483

ID ADK63215 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #733.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.

Query Match 0.8%; Score 18; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 484

ID AAS87283 standard; cDNA; 2047 BP.
DE DNA encoding novel human diagnostic protein #23087.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 5; Length 2047;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 485

ID ABT31747 standard; DNA; 2152 BP.
DE GAAP-1 related DNA sequence #1.
PN WO200298916-A2.
PD 12-DEC-2002.

PA (CNRS) CENT NAT RECH SCI.

Query Match 0.8%; Score 18; DB 8; Length 2152;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 486

ID ABT31749 standard; DNA; 2178 BP.

DE GAAP-1 related DNA sequence #3.

PN WO200298916-A2.

PD 12-DEC-2002.

PA (CNRS) CENT NAT RECH SCI.

Query Match 0.8%; Score 18; DB 8; Length 2178;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 487

ID ACC46342 standard; cDNA; 2179 BP.

DE Human dithp zinc finger transcriptional regulator-encoding cDNA.

PN WO200297031-A2.

PD 05-DEC-2002.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 8; Length 2179;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 488

ID ADE31311 standard; DNA; 2179 BP.

DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 66.

PN WO2003062376-A2.

PD 31-JUL-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 10; Length 2179;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 489

ID ADB62959 standard; cDNA; 2228 BP.

DE Human cDNA encoding clone PROST20007170.

PN EP1308459-A2.

PD 07-MAY-2003.

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 0.8%; Score 18; DB 10; Length 2228;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 490

ID AAH16583 standard; cDNA; 2338 BP.

DE Human cDNA sequence SEQ ID NO:15667.

PN EP1074617-A2.

PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.

Query Match 0.8%; Score 18; DB 4; Length 2338;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 491

ID AAH18401 standard; cDNA; 2362 BP.

DE Human cDNA sequence SEQ ID NO:18465.

PN EP1074617-A2.

PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.

Query Match 0.8%; Score 18; DB 4; Length 2362;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 492

ID AAS81549 standard; cDNA; 2418 BP.

DE DNA encoding novel human diagnostic protein #17353.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 5; Length 2418;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 493

ID AAH16233 standard; cDNA; 2492 BP.

DE Human cDNA sequence SEQ ID NO:15059.

PN EP1074617-A2.

PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.

Query Match 0.8%; Score 18; DB 4; Length 2492;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 494

ID ADA84026 standard; DNA; 2492 BP.

DE Human POM94 gene.

PN WO2002103028-A2.

PD 27-DEC-2002.

PA (BIOM-) BIOMEDICAL CENT.

Query Match 0.8%; Score 18; DB 8; Length 2492;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 495

ID ADB53889 standard; DNA; 2497 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4431.

PN WO2003065993-A2.

PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 0.8%; Score 18; DB 10; Length 2497;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 496

ID ABL09142 standard; cDNA; 2498 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21908.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 0.8%; Score 18; DB 4; Length 2498;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 497

ID ABZ24410 standard; cDNA; 2576 BP.

DE Human TBC1D1 nucleic acid 5689552.

PN WO200299049-A2.

PD 12-DEC-2002.

PA (EXEL-) EXELIXIS INC.

Query Match 0.8%; Score 18; DB 8; Length 2576;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 498

ID ADR24190 standard; DNA; 2576 BP.

DE Breast cancer prognosis marker #51.

PN WO2004065545-A2.

PD 05-AUG-2004.

PA (ROSE-) ROSETTA INPHARMATICS LLC.

PA (NECA-) NETHERLANDS CANCER INST.

Query Match 0.8%; Score 18; DB 13; Length 2576;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 499

ID AAD15300 standard; cDNA; 2589 BP.

DE Human PMS2 cDNA.

PN WO200161012-A1.

PD 23-AUG-2001.

PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
PA (KINZ/) KINZLER K.
PA (VOGE/) VOGELSTEIN B.

Query Match 0.8%; Score 18; DB 4; Length 2589;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 500

ID AAQ90940 standard; DNA; 2687 BP.
DE Human wild type PMS1 gene, a MutL homologue.
PN WO9516793-A1.
PD 22-JUN-1995.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.

Query Match 0.8%; Score 18; DB 2; Length 2687;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 501

ID AAQ14790 standard; cDNA; 2745 BP.
DE Haemonchus contortus phosphofructokinase gene.
PN WO9117260-A.
PD 14-NOV-1991.
PA (UPJO) UPJOHN CO.

Query Match 0.8%; Score 18; DB 2; Length 2745;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 502

ID AAQ97527 standard; cDNA; 2771 BP.
DE Human DNA repair protein hMLH3 coding sequence.
PN WO9520678-A1.
PD 03-AUG-1995.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 18; DB 2; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 503

ID AAZ59955 standard; cDNA; 2771 BP.
DE cDNA encoding wild-type human mismatch repair enzyme PMS2.
PN CA2240609-A1.
PD 14-OCT-1999.
PA (UYJO) UNIV JOHNS HOPKINS.

Query Match 0.8%; Score 18; DB 3; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 504

ID AAZ59956 standard; cDNA; 2771 BP.
DE cDNA encoding dominant negative PMS2 allele hPMS2-134.
PN CA2240609-A1.
PD 14-OCT-1999.
PA (UYJO) UNIV JOHNS HOPKINS.

Query Match 0.8%; Score 18; DB 3; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 505

ID AAH76364 standard; cDNA; 2771 BP.
DE Human PMS2 cDNA.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.

Query Match 0.8%; Score 18; DB 4; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 506

ID AAH75041 standard; cDNA; 2771 BP.
 DE Nucleotide sequence of human mismatch repair protein PMS2.
 PN WO200162945-A1.
 PD 30-AUG-2001.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (NICO/) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 PA (GRAS/) GRASSO L.
 PA (VOGE/) VOGELSTEIN B.
 PA (KINZ/) KINZLER K W.
 Query Match 0.8%; Score 18; DB 5; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 507
 ID ABK86088 standard; DNA; 2771 BP.
 DE Human cDNA encoding post meiotic segregation increased, PMS2.
 PN WO200238750-A1.
 PD 16-MAY-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 508
 ID AAD39197 standard; cDNA; 2771 BP.
 DE Human mismatch repair protein, PMS2 cDNA.
 PN WO200237967-A1.
 PD 16-MAY-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 509
 ID AAL48697 standard; DNA; 2771 BP.
 DE Human mismatch repair protein PMS2 coding sequence.
 PN WO200254856-A1.
 PD 18-JUL-2002.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 510
 ID AAD45355 standard; cDNA; 2771 BP.
 DE Human MLH3 cDNA.
 PN US6416984-B1.
 PD 09-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 511
 ID AAD45434 standard; cDNA; 2771 BP.
 DE Human MLH3 mutant cDNA #1.
 PN US6416984-B1.
 PD 09-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 512
 ID AAD39769 standard; cDNA; 2771 BP.
 DE Human PMS2 cDNA.
 PN WO200240499-A1.
 PD 23-MAY-2002.

PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 6; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 513
 ID ABX12939 standard; DNA; 2771 BP.
 DE DNA encoding human PMS2 protein.
 PN WO2003012130-A1.
 PD 13-FEB-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 8; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 514
 ID ACA89703 standard; cDNA; 2771 BP.
 DE cDNA encoding human PMS2 mismatch repair protein.
 PN WO2003031937-A2.
 PD 17-APR-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 8; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 515
 ID ACD13763 standard; cDNA; 2771 BP.
 DE Human MutL homologue, hMLH3, cDNA.
 PN US2003027177-A1.
 PD 06-FEB-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 0.8%; Score 18; DB 9; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 516
 ID AAL57763 standard; cDNA; 2771 BP.
 DE Human mismatch repair protein PMS (post meiotic segregation) 2 cDNA.
 PN WO2003062435-A1.
 PD 31-JUL-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 9; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 517
 ID ADA06243 standard; DNA; 2771 BP.
 DE DNA encoding the human mismatch repair, MMR, protein PMS2.
 PN US2003068808-A1.
 PD 10-APR-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 PA (GRAS/) GRASSO L.
 PA (KLIN/) KLINE J B.
 Query Match 0.8%; Score 18; DB 9; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 518
 ID ADC89606 standard; cDNA; 2771 BP.
 DE Human PMS2 encoding cDNA SEQ ID NO:5.
 PN WO2003072732-A2.
 PD 04-SEP-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 10; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 519
 ID ADF17891 standard; DNA; 2771 BP.
 DE Human PMS2 cDNA, a mismatch repair gene.

PN US6576468-B1.
 PD 10-JUN-2003.
 PA (MORP-) MORPHOTEK INC.
 Query Match 0.8%; Score 18; DB 10; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 520
 ID ADG62891 standard; cDNA; 2771 BP.
 DE Human PMS2 cDNA.
 PN US2003165468-A1.
 PD 04-SEP-2003.
 PA (GRAS/) GRASSO L.
 PA (NICO/) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 10; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 521
 ID ADH62628 standard; cDNA; 2771 BP.
 DE Human mismatch repair protein PMS2 cDNA.
 PN US2003143682-A1.
 PD 31-JUL-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 10; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 522
 ID ADH60984 standard; cDNA; 2771 BP.
 DE Human cDNA encoding mismatch repair protein hMLH3.
 PN US6610477-B1.
 PD 26-AUG-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 0.8%; Score 18; DB 10; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 523
 ID ADF78839 standard; cDNA; 2771 BP.
 DE Human mismatch repair protein PMS2.
 PN US2003186441-A1.
 PD 02-OCT-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 12; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 524
 ID ADG46766 standard; cDNA; 2771 BP.
 DE Human MMR protein (mismatch protein), PMS2 cDNA.
 PN US2003091997-A1.
 PD 15-MAY-2003.
 PA (NICO/) NICOLAIDES N C.
 PA (GRAS/) GRASSO L.
 PA (SASS/) SASS P M.
 Query Match 0.8%; Score 18; DB 12; Length 2771;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 RESULT 525
 ID ADO40065 standard; cDNA; 2771 BP.
 DE Human PMS2 cDNA.

PN US6737268-B1.
PD 18-MAY-2004.
PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 12; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 526

ID ADP12816 standard; DNA; 2771 BP.
DE Reference mRNA sequence #30.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

Query Match 0.8%; Score 18; DB 12; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 527

ID ADP66681 standard; DNA; 2771 BP.
DE Human mismatch repair protein PMS2 encoding DNA.
PN WO2004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 12; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 528

ID ADQ87551 standard; cDNA; 2771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4429.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 0.8%; Score 18; DB 12; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 529

ID ADQ87314 standard; cDNA; 2771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4191.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 0.8%; Score 18; DB 13; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 530

ID ADR13882 standard; cDNA; 2771 BP.
DE Human DNA mismatch repair protein PMS2 cDNA.
PN US2004158886-A1.
PD 12-AUG-2004.
PA (MORP-) MORPHOTEK INC.

Query Match 0.8%; Score 18; DB 13; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 531

ID ACN41774 standard; cDNA; 2787 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:649.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 0.8%; Score 18; DB 13; Length 2787;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 532

ID ADR07917 standard; cDNA; 2890 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1423.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 0.8%; Score 18; DB 13; Length 2890;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 533

ID ABQ55018 standard; cDNA; 2897 BP.
DE Human ovarian antigen HTGFW12 cDNA, SEQ ID NO:898.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 18; DB 6; Length 2897;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 534

ID ADR07498 standard; cDNA; 2988 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1004.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 0.8%; Score 18; DB 13; Length 2988;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 535

ID AAK94796 standard; cDNA; 2989 BP.
DE Human full-length cDNA, SEQ ID NO: 3914.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.

Query Match 0.8%; Score 18; DB 4; Length 2989;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 536

ID ADL31881 standard; cDNA; 2989 BP.
DE Full length human cDNA clone SeqID 3914.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 0.8%; Score 18; DB 12; Length 2989;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 537

ID AAS81539 standard; cDNA; 3006 BP.
DE DNA encoding novel human diagnostic protein #17343.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 5; Length 3006;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 538

ID ABZ24412 standard; cDNA; 3023 BP.
DE Human TBC1D1 nucleic acid 17939551.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 0.8%; Score 18; DB 8; Length 3023;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 539

ID ABL23724 standard; DNA; 3137 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 22645.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 0.8%; Score 18; DB 4; Length 3137;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 540

ID ADL14038 standard; cDNA; 3258 BP.
DE Human cDNA encoding sarcoma-associated antigen NY-SAR-5.
PN US2004063101-A1.
PD 01-APR-2004.
PA (SCAN/) SCANLAN M J.
PA (LEES/) LEE S.
PA (OLDL/) OLD L J.

Query Match 0.8%; Score 18; DB 12; Length 3258;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 541

ID AAI59640 standard; cDNA; 3281 BP.
DE Human polynucleotide SEQ ID NO 3629.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 4; Length 3281;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 542

ID ABX05239 standard; cDNA; 3317 BP.
DE Human novel polynucleotide #254.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 8; Length 3317;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 543

ID AAI57854 standard; cDNA; 3326 BP.
DE Human polynucleotide SEQ ID NO 57.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 18; DB 4; Length 3326;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 544

ID ADB80378 standard; DNA; 3332 BP.
DE Human MDDT gene SEQ ID NO:65.
PN WO2003016497-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 9; Length 3332;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 545

ID ADQ18716 standard; DNA; 3367 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1535.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 0.8%; Score 18; DB 12; Length 3367;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 546

ID ABT42727 standard; DNA; 3381 BP.
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:8.
PN WO2002103017-A1.
PD 27-DEC-2002.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 0.8%; Score 18; DB 8; Length 3381;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 547

ID ABV29011 standard; cDNA; 3382 BP.
DE Human prostate expression marker cDNA 29002.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 3382;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 548

ID ABV23171 standard; cDNA; 3382 BP.
DE Human prostate expression marker cDNA 23162.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 3382;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 549

ID AAZ27622 standard; DNA; 3496 BP.
DE Plasmid TOPI-1.
PN WO9949063-A1.
PD 30-SEP-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 0.8%; Score 18; DB 2; Length 3496;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 550

ID ADM47670 standard; DNA; 3501 BP.
DE Polynucleotide sequence #88 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 0.8%; Score 18; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 551

ID ADM18411 standard; DNA; 3512 BP.
DE Human chromosome 1ptel subtelomeric DNA probe SEQ ID NO:35.
PN WO2004029283-A2.
PD 08-APR-2004.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 0.8%; Score 18; DB 12; Length 3512;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 552

ID ACC46686 standard; cDNA; 3607 BP.
DE Human dithp biochemical pathway protein-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 8; Length 3607;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 553

ID ADE57649 standard; DNA; 3640 BP.
DE Human gene J00265, SEQ ID NO 3511.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match 0.8%; Score 18; DB 10; Length 3640;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 554

ID ADA70734 standard; DNA; 3645 BP.
DE Rice gene, SEQ ID 4057.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 0.8%; Score 18; DB 8; Length 3645;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 555

ID ADQ64879 standard; cDNA; 3646 BP.
DE Novel human cDNA sequence #2040.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 0.8%; Score 18; DB 12; Length 3646;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 556

ID ADI57183 standard; cDNA; 3663 BP.
DE Human PLC-betal encoding cDNA SEQ ID NO:3.
PN WO2004007754-A2.
PD 22-JAN-2004.
PA (RIGE-) RIGEL PHARM INC.

Query Match 0.8%; Score 18; DB 12; Length 3663;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 557

ID ABA96004 standard; cDNA; 3700 BP.
DE Human lipid metabolism enzyme-4 (LME-4) cDNA.
PN WO200185956-A2.
PD 15-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 6; Length 3700;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 558

ID AAC77404 standard; cDNA; 3727 BP.
DE Human ORFX ORF2959 polynucleotide sequence SEQ ID NO:5917.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.

Query Match 0.8%; Score 18; DB 3; Length 3727;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 559

ID ADJ80212 standard; cDNA; 3737 BP.
DE Novel human nucleic acid-associated protein coding sequence #30.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 10; Length 3737;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 560

ID ABL90217 standard; cDNA; 3751 BP.
 DE Human polynucleotide SEQ ID NO 779.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 0.8%; Score 18; DB 6; Length 3751;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 561

ID AAZ27621 standard; DNA; 3766 BP.
 DE Plasmid TOP-1.
 PN WO9949063-A1.
 PD 30-SEP-1999.
 PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.

Query Match 0.8%; Score 18; DB 2; Length 3766;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 562

ID ADS47565 standard; cDNA; 3822 BP.
 DE Bacterial polynucleotide #2308.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

Query Match 0.8%; Score 18; DB 13; Length 3822;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 563

ID ABL14239 standard; cDNA; 3924 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37199.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.

Query Match 0.8%; Score 18; DB 4; Length 3924;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 564

ID AAZ50906 standard; cDNA; 3983 BP.
 DE Human TBC-1 cDNA from first transcript.
 PN WO200008209-A2.
 PD 17-FEB-2000.
 PA (GEST) GENSET.

Query Match 0.8%; Score 18; DB 3; Length 3983;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 565

ID ABZ24414 standard; cDNA; 3983 BP.
 DE Human TBC1D1 1st transcript.
 PN WO200299049-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.

Query Match 0.8%; Score 18; DB 8; Length 3983;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 566

ID AAZ50907 standard; cDNA; 3988 BP.
 DE Human TBC-1 cDNA from second transcript.